

GenCore version 5.1.6
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Om protein - protein search, using sw model
Run on: October 26, 2005, 08:01:20 ; Search time 127.778 Seconds
(without alignments)
20.038 Million cell updates/sec

Title: US-10-053-669-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum_DB_seq_length:=0
Maximum_DB_seq_length:=200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt 03.1;
1: uniprot_sprot:*,
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|------------------------|
| 1 | 27 | 100.0 | 11 | 1 TNA4_PSEGU | PA2989 pseudophryn |
| 2 | 27 | 100.0 | 11 | 1 TNA5_PSEGU | PA2990 pseudophryn |
| 3 | 27 | 100.0 | 11 | 1 TNA1_CAVPO | PA67932 cavia porce |
| 4 | 27 | 100.0 | 11 | 1 TNA1_CHICK | PI9850 gallus galli |
| 5 | 27 | 100.0 | 11 | 1 TNA1_HORSE | PI67933 equus cabal |
| 6 | 27 | 100.0 | 11 | 1 TNA1_ONCML | PI84949 oncorhynchus |
| 7 | 27 | 100.0 | 11 | 1 TNA1_SCYCA | PA1333 scylliorhinus |
| 8 | 27 | 100.0 | 45 | 2 Q6LD03 | Q6LD03 rattus sp. |
| 9 | 27 | 100.0 | 1 | 1 YATL_RHOBL | PO5443 rhodopsin |
| 10 | 27 | 100.0 | 72 | 2 QYJY54 | QYJY54 homo sapien |
| 11 | 27 | 100.0 | 74 | 2 Q8IWZ7 | Q8IWZ7 homo sapien |
| 12 | 27 | 100.0 | 76 | 2 Q8EJU6 | Q8EJU6 homo sapien |
| 13 | 27 | 100.0 | 82 | 2 Q6CK5 | Q6CK5 oryctolagus |
| 14 | 27 | 100.0 | 87 | 2 Q8EJU7 | Q8EJU7 homo sapien |
| 15 | 27 | 100.0 | 96 | 2 Q8EJU8 | Q8EJU8 homo sapien |
| 16 | 27 | 100.0 | 99 | 2 Q9RD07 | Q9RD07 streptomyce |
| 17 | 27 | 100.0 | 100 | 2 Q6CK6 | Q6CK6 oryctolagus |
| 18 | 27 | 100.0 | 104 | 2 Q7VCI2 | Q7VCI2 prochlorococcus |
| 19 | 27 | 100.0 | 107 | 2 Q6CK8 | Q6CK8 homo sapien |
| 20 | 27 | 100.0 | 107 | 2 Q8EJU7 | Q8EJU7 homo sapien |
| 21 | 27 | 100.0 | 108 | 2 Q8FWTO | Q8FWTO brucella su |
| 22 | 27 | 100.0 | 113 | 2 Q8EWU9 | Q8EWU9 homo sapien |
| 23 | 27 | 100.0 | 114 | 2 Q97947 | Q97947 tupaias glis |
| 24 | 27 | 100.0 | 115 | 1 TKN1_RABIT | PA1540 oryctolagus |
| 25 | 27 | 100.0 | 115 | 2 Q9XIV2 | Q9XIV2 thermotoga |
| 26 | 27 | 100.0 | 119 | 2 Q94QPS | Q94QPS inversibidens |
| 27 | 27 | 100.0 | 124 | 2 Q9CGC7 | Q9CGC7 lactococcus |
| 28 | 27 | 100.0 | 129 | 1 TKN1_HUMAN | PO3366 homo sapien |
| 29 | 27 | 100.0 | 129 | 2 Q97948 | Q97948 tupaias glis |
| 30 | 27 | 100.0 | 130 | 1 TKN1_BOVIN | PO1289 bos tauruis |
| 31 | 27 | 100.0 | 130 | 1 TKN1_MESAU | Q60541 mesocricetus |

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Om protein - protein search, using BW model

Run on:

October 26, 2005, 08:04:16 ; Search time 13.3333 Seconds

(without alignments)

36.081 Million cell updates/sec

Title: US-10-053-669-1

Perfect score: 27

Sequence: 1 FFGLM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0%

Database : 233416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum_DB_seq_length: 0

Maximum_DB_seq_length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

LISTING FIRST 150 SUMMARIES

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|----------|------------------------------|
| 1 | 27 | 100.0 | 11 | A60654 | substance P - guin |
| 2 | 27 | 100.0 | 11 | SPHO | substance P - hors |
| 3 | 27 | 100.0 | 11 | JN0023 | substance P - chic |
| 4 | 27 | 100.0 | 11 | S33300 | probable substance |
| 5 | 27 | 100.0 | 11 | E60409 | substance P-like P |
| 6 | 27 | 100.0 | 11 | F60409 | substance P-like P |
| 7 | 27 | 100.0 | 11 | S22308 | substance P - rain |
| 8 | 27 | 100.0 | 63 | JC2412 | tachykinin gamma C |
| 9 | 27 | 100.0 | 69 | S04666 | hypothetical prote |
| 10 | 27 | 100.0 | 72 | JCG455 | proprotein tachykinin-A |
| 11 | 27 | 100.0 | 72 | I62742 | tachykinin A gamma |
| 12 | 27 | 100.0 | 97 | S12958 | tachykinin delta p |
| 13 | 27 | 100.0 | 112 | SPRTA | substance P alpha |
| 14 | 27 | 100.0 | 115 | SPRBG | substance P gamma |
| 15 | 27 | 100.0 | 115 | I47039 | tachykinin 1 precur |
| 16 | 27 | 100.0 | 116 | C72232 | hypothetical prote |
| 17 | 27 | 100.0 | 124 | B86771 | tachykinin A gamma |
| 18 | 27 | 100.0 | 129 | 1 SPHOB | tachykinin delta p |
| 19 | 27 | 100.0 | 130 | 1 SPRTB | substance P alpha |
| 20 | 27 | 100.0 | 130 | 1 SPRTB | substance P gamma |
| 21 | 27 | 100.0 | 130 | S47038 | tachykinin 1 precur |
| 22 | 27 | 100.0 | 130 | 2 I52526 | hypothetical prote |
| 23 | 27 | 100.0 | 166 | 2 AG1931 | tachykinin 1 precur |
| 24 | 27 | 100.0 | 173 | 1 B83931 | neurokinin 1 precur |
| 25 | 27 | 100.0 | 173 | 1 H64634 | neurokinin 1 precur |
| 26 | 27 | 100.0 | 230 | 2 F71879 | hypothetical prote |
| 27 | 27 | 100.0 | 234 | 2 PT5254 | conserved hypothetical prote |
| 28 | 27 | 100.0 | 256 | 2 D81181 | conserved hypothetical prote |
| 29 | 100.0 | | 256 | 2 C81925 | probable sec-indep |

IS0963-4 transpos

IS0963-6 transpos

IS0963-3 transpos

IS0963-2 transpos

transporter, dme f

probable transport

IS0963-5 transpos

hypothetical prote

desmocollin - bovi

hypothetical prote

glycoprotein vp260

hypothetical prote

phosphoribosylamin

proline transpor

hypothetical prote

hypothetical prote

best protein homol

hypothetical prote

conserved hypothet

hypothetical prote

cillate transpor

hypothetical prote

potassium channel

hypothetical prote

probable fatty-aci

becl9 protein homol

protein P22G5.32 [

ABC transporter (P

v-type sodium ATP

ntp protein - Ent

H+-transporting AT

1594 protein - fis

heavy-metal transp

hypothetical prote

genome polyprotein

genome

sialokinin II - ye

sialokinin I - yel

scylliorhinin I - g

ranatacykinin B -

uperolein - frog (

physalaemin - frog

ranatacykinin A -

protoosystem II pro

hypothetical prote

B-ORF-B protein -

B2L protein - vari

hypothetical prote

hypothetical prote

hypothetical prote

hypothetical prote

hypothetical prote

hypothetical prote

ribosomal protein

hypothetical prote

| | | | Matches | 5; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|---|----|------|---------|----|--------------|----|------------|----|--------|----|------|----|
| 103 | 24 | 88.9 | 161 | 2 | F83322 | | | | | | | |
| 104 | 24 | 88.9 | 167 | 2 | G90175 | | | | | | | |
| 105 | 24 | 88.9 | 169 | 2 | D87294 | | | | | | | |
| 106 | 24 | 88.9 | 172 | 2 | AE283 | | | | | | | |
| 107 | 24 | 88.9 | 178 | 2 | J53337 | | | | | | | |
| 108 | 24 | 88.9 | 178 | 2 | S07337 | | | | | | | |
| 109 | 24 | 88.9 | 183 | 2 | T43337 | | | | | | | |
| 110 | 24 | 88.9 | 185 | 2 | A61159 | | | | | | | |
| 111 | 24 | 88.9 | 189 | 2 | C90592 | | | | | | | |
| 112 | 24 | 88.9 | 197 | 2 | E90111 | | | | | | | |
| 113 | 24 | 88.9 | 197 | 2 | H97882 | | | | | | | |
| 114 | 24 | 88.9 | 204 | 2 | G83904 | | | | | | | |
| 115 | 24 | 88.9 | 206 | 2 | C70226 | | | | | | | |
| 116 | 24 | 88.9 | 215 | 2 | JX0244 | | | | | | | |
| 117 | 24 | 88.9 | 215 | 2 | S22432 | | | | | | | |
| 118 | 24 | 88.9 | 217 | 2 | C90525 | | | | | | | |
| 119 | 24 | 88.9 | 217 | 2 | A83840 | | | | | | | |
| 120 | 24 | 88.9 | 218 | 2 | S73626 | | | | | | | |
| 121 | 24 | 88.9 | 219 | 2 | D70411 | | | | | | | |
| 122 | 24 | 88.9 | 220 | 2 | AD225 | | | | | | | |
| 123 | 24 | 88.9 | 222 | 2 | AB0750 | | | | | | | |
| 124 | 24 | 88.9 | 222 | 2 | A83809 | | | | | | | |
| 125 | 24 | 88.9 | 222 | 2 | H99960 | | | | | | | |
| 126 | 24 | 88.9 | 222 | 2 | C63955 | | | | | | | |
| 127 | 24 | 88.9 | 224 | 2 | C62420 | | | | | | | |
| 128 | 24 | 88.9 | 227 | 2 | D86331 | | | | | | | |
| 129 | 24 | 88.9 | 227 | 2 | G83704 | | | | | | | |
| 130 | 24 | 88.9 | 228 | 2 | AE1704 | | | | | | | |
| 131 | 24 | 88.9 | 228 | 2 | AF3333 | | | | | | | |
| 132 | 24 | 88.9 | 232 | 2 | A84053 | | | | | | | |
| 133 | 24 | 88.9 | 233 | 2 | A87601 | | | | | | | |
| 134 | 24 | 88.9 | 234 | 2 | B61544 | | | | | | | |
| 135 | 24 | 88.9 | 235 | 2 | T28882 | | | | | | | |
| 136 | 24 | 88.9 | 239 | 2 | JCT752 | | | | | | | |
| 137 | 24 | 88.9 | 244 | 2 | A65052 | | | | | | | |
| 138 | 24 | 88.9 | 255 | 2 | AG1198 | | | | | | | |
| 139 | 24 | 88.9 | 255 | 2 | AE1556 | | | | | | | |
| 140 | 24 | 88.9 | 264 | 2 | A71367 | | | | | | | |
| 141 | 24 | 88.9 | 264 | 2 | T31551 | | | | | | | |
| 142 | 24 | 88.9 | 265 | 2 | A84937 | | | | | | | |
| 143 | 24 | 88.9 | 272 | 2 | C8642 | | | | | | | |
| 144 | 24 | 88.9 | 272 | 2 | C86884 | | | | | | | |
| 145 | 24 | 88.9 | 272 | 2 | D8671 | | | | | | | |
| 146 | 24 | 88.9 | 275 | 2 | E75548 | | | | | | | |
| 147 | 24 | 88.9 | 276 | 2 | A49853 | | | | | | | |
| 148 | 24 | 88.9 | 282 | 2 | T13393 | | | | | | | |
| 149 | 24 | 88.9 | 284 | 2 | T33860 | | | | | | | |
| 150 | 24 | 88.9 | 287 | 2 | C84567 | | | | | | | |
| ALIGNMENTS | | | | | | | | | | | | |
| RESULT 1 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
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| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |
| A6054 A;Title: Primary amino acid sequence of guinea-pig substance P. A;Reference number: A6054; MUID:9044685; PMID:2478925 | | | | | | | | | | | | |
| C;Species: <i>Cavia porcellus</i> (guinea pig) C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| R;MultiPPY_R. Neuropeptides 14, 105-110, 1989 | | | | | | | | | | | | |

GenCore version 5.1.6
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Om protein - protein search, using sw model
Run on: October 26, 2005, 08:05:47 ; Search time 124.444 seconds
Title: US-10-053-669-1
Perfect score: 27
Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Maximum_DB_seq_length: 0
(Maximum_DB_seq_length: 2000000000)

Searched: 1862994 seqs, 417510619 residues
Total number of hits satisfying chosen parameters: 1862994
Minimum_DB_seq_length: 0
Post-processing: Maximum Match 0%
Listing first 150 summaries

Database : Published Applications AA.*
1: /cgmn_6_ptodata/1/pubpaas/US07_PUBCOMB.pep: *
2: /cgmn_6_ptodata/1/pubpaas/PCIT_NEW_PUB.pep: *
3: /cgmn_6_ptodata/1/pubpaas/US06_NEW_PUBCOMB.pep: *
4: /cgmn_6_ptodata/1/pubpaas/US06_PUBCOMB.pep: *
5: /cgmn_6_ptodata/1/pubpaas/US07_NEW_PUB.pep: *
6: /cgmn_6_ptodata/1/pubpaas/PCTRS_PUBCOMB.pep: *
7: /cgmn_6_ptodata/1/pubpaas/US07_NEW_PUB.pep: *
8: /cgmn_6_ptodata/1/pubpaas/US08_PUBCOMB.pep: *
9: /cgmn_6_ptodata/1/pubpaas/US10C_PUBCOMB.pep: *
10: /cgmn_6_ptodata/1/pubpaas/US09_PUBCOMB.pep: *
11: /cgmn_6_ptodata/1/pubpaas/US09C_PUBCOMB.pep: *
12: /cgmn_6_ptodata/1/pubpaas/US09_NEW_PUB.pep: *
13: /cgmn_6_ptodata/1/pubpaas/US10_PUBCOMB.pep: *
14: /cgmn_6_ptodata/1/pubpaas/US10B_PUBCOMB.pep: *
15: /cgmn_6_ptodata/1/pubpaas/US10C_PUBCOMB.pep: *
16: /cgmn_6_ptodata/1/pubpaas/US10_PUBCOMB.pep: *
17: /cgmn_6_ptodata/1/pubpaas/US10E_PUBCOMB.pep: *
18: /cgmn_6_ptodata/1/pubpaas/US10_NEW_PUB.pep: *
19: /cgmn_6_ptodata/1/pubpaas/US11A_PUBCOMB.pep: *
20: /cgmn_6_ptodata/1/pubpaas/US11C_PUBCOMB.pep: *
21: /cgmn_6_ptodata/1/pubpaas/US60_NEW_PUB.pep: *
22: /cgmn_6_ptodata/1/pubpaas/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query | # | Length | DB ID | Description |
|------------|-------|-------|---|--------|-------------------|---------------------|
| 1 | 27 | 100.0 | 5 | 9 | US-09-265-690-1 | Sequence 1, Appli |
| 2 | 27 | 100.0 | 5 | 14 | US-10-053-669-1 | Sequence 1, Appli |
| 3 | 27 | 100.0 | 5 | 15 | US-10-134-187-3 | Sequence 3, Appli |
| 4 | 27 | 100.0 | 5 | 16 | US-10-688-741-3 | Sequence 3, Appli |
| 5 | 27 | 100.0 | 5 | 16 | US-10-805-881-1 | Sequence 1, Appli |
| 6 | 27 | 100.0 | 5 | 16 | US-10-720-030-3 | Sequence 3, Appli |
| 7 | 27 | 100.0 | 5 | 17 | US-10-497-620-15 | Sequence 15, Appli |
| 8 | 27 | 100.0 | 5 | 20 | US-11-056-697-604 | Sequence 604, Appli |
| 9 | 27 | 100.0 | 5 | 20 | US-11-025-494-3 | Sequence 3, Appli |
| 10 | 27 | 100.0 | 6 | 14 | US-10-688-788-38 | Sequence 38, Appli |
| 11 | 27 | 100.0 | 6 | 17 | US-10-497-628-14 | Sequence 14, Appli |

| | | | | | | |
|----|----|-------|----|----|-------------------|---------------------|
| 12 | 27 | 100.0 | 6 | 20 | US-11-066-697-595 | Sequence 595, App |
| 13 | 27 | 100.0 | 6 | 20 | US-11-066-697-597 | Sequence 597, App |
| 14 | 27 | 100.0 | 6 | 20 | US-11-066-697-601 | Sequence 601, App |
| 15 | 27 | 100.0 | 7 | 14 | US-10-036-542-110 | Sequence 110, App |
| 16 | 27 | 100.0 | 7 | 14 | US-10-036-542-111 | Sequence 111, App |
| 17 | 27 | 100.0 | 7 | 14 | US-10-036-542-111 | Sequence 37, App |
| 18 | 27 | 100.0 | 7 | 15 | US-10-134-187-2 | Sequence 2, Appli |
| 19 | 27 | 100.0 | 7 | 16 | US-10-688-711-2 | Sequence 2, Appli |
| 20 | 27 | 100.0 | 7 | 16 | US-10-720-039-2 | Sequence 2, Appli |
| 21 | 27 | 100.0 | 7 | 17 | US-10-497-628-13 | Sequence 13, Appli |
| 22 | 27 | 100.0 | 7 | 20 | US-11-066-697-596 | Sequence 596, App |
| 23 | 27 | 100.0 | 7 | 20 | US-11-066-697-597 | Sequence 607, App |
| 24 | 27 | 100.0 | 7 | 20 | US-11-025-494-2 | Sequence 2, Appli |
| 25 | 27 | 100.0 | 8 | 14 | US-10-168-789A-36 | Sequence 36, Appli |
| 26 | 27 | 100.0 | 8 | 17 | US-10-497-628-12 | Sequence 12, Appli |
| 27 | 27 | 100.0 | 8 | 20 | US-11-066-697-583 | Sequence 583, App |
| 28 | 27 | 100.0 | 8 | 20 | US-11-066-697-592 | Sequence 592, App |
| 29 | 27 | 100.0 | 9 | 20 | US-11-066-697-600 | Sequence 600, App |
| 30 | 27 | 100.0 | 9 | 20 | US-11-036-542-112 | Sequence 622, App |
| 31 | 27 | 100.0 | 9 | 20 | US-11-025-494-1 | Sequence 1, Appli |
| 32 | 27 | 100.0 | 9 | 20 | US-10-134-187-1 | Sequence 1, Appli |
| 33 | 27 | 100.0 | 9 | 16 | US-10-688-741-1 | Sequence 1, Appli |
| 34 | 27 | 100.0 | 9 | 20 | US-10-720-039-1 | Sequence 1, Appli |
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; Publication No. US20010051345A1
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; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: 1427001
; CURRENT APPLICATION NUMBER: US/09/265, 690C
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
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; CURRENT APPLICATION NUMBER: US/10/053, 669
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; Publication No. US20030202981A1
; GENERAL INFORMATION:
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; APPLICANT: Kream, Richard M.
; TITLE OF INVENTION: Chimeric Hybrid Analgesics

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| | | | | | Sequence 10, Appli |
| | | | | | Sequence 10, Appli |
| | | | | | Sequence 24, Appli |
| | | | | | Sequence 27, Appli |
| | | | | | Sequence 30, Appli |
| | | | | | Sequence 1, Appli |
| | | | | | Sequence 2, Appli |
| | | | | | Sequence 50, Appli |
| | | | | | Sequence 50, Appli |
| | | | | | Sequence 23, Appli |
| | | | | | Sequence 4, Appli |

APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/105,071
APPLICATION NUMBER: US 07/934,553
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide

ALIGNMENTS

RESULT 1
US-07-934-553-2
Sequence 2, Application US/07934553
; Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, Fallon, LUM
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:

RESULT 1
US-07-934-553-2
Sequence 2, Application US/07934553
Patent No. 5314590
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE PREPARATION OF ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALCON LUMBER COMPANY
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:

Om protein - protein search, using BW model.

Run on: October 26, 2005, 08:00:50 ; Search time 72.2222 seconds
 26.776 Million cell updates/sec

Title: US-10-053-669-1

Perfect score: 27

Sequence: 1 FFGLM 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum_DB_seq_length=0

Maximum_DB_seq_length=200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 150 summaries

Database : A_GenSeq_16Dec04:*

- 1: geneSeq1980s:*
- 2: geneSeq1990s:*
- 3: geneSeq2000s:*
- 4: geneSeq201s:*
- 5: geneSeq2002s:*
- 6: geneSeq2003s:*
- 7: geneSeq2004s:*
- 8: geneSeq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 27 | 100.0 | 5 | AAR33009 | Aar33009 Alpha-sab |
| 2 | 27 | 100.0 | 5 | AAR33008 | Aar33008 Alpha-sab |
| 3 | 27 | 100.0 | 5 | AAR33007 | Aar33007 Alpha-sab |
| 4 | 27 | 100.0 | 5 | AAR33010 | Aar33010 Alpha-sab |
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| 6 | 27 | 100.0 | 5 | AAR34551 | Aar34551 Cholecyt |
| 7 | 27 | 100.0 | 5 | AAR34550 | Aar34550 Cholecyt |
| 8 | 27 | 100.0 | 5 | AAR34548 | Aar34548 Cholecyt |
| 9 | 27 | 100.0 | 5 | AAR1687 | Aar1687 Tetracypt |
| 10 | 27 | 100.0 | 5 | AAR99643 | Aar99643 Substance |
| 11 | 27 | 100.0 | 5 | AAY50325 | Aay50325 Neutrophil |
| 12 | 27 | 100.0 | 5 | AAY2660 | Aay2660 Human tac |
| 13 | 27 | 100.0 | 5 | AAB23025 | Aab23025 Human/rat |
| 14 | 27 | 100.0 | 5 | AY67576 | Ay67576 P antagon |
| 15 | 27 | 100.0 | 5 | AAY91428 | Aay91428 Tachykini |
| 16 | 27 | 100.0 | 5 | ABP10088 | Abp10088 Substance |
| 17 | 27 | 100.0 | 5 | AAP77845 | Aap77845 Tachykini |
| 18 | 27 | 100.0 | 5 | ADE9203 | Ade9203 High acti |
| 19 | 27 | 100.0 | 5 | ADP2530 | Adp2530 Substance |
| 20 | 27 | 100.0 | 5 | ADN5078 | Adn5078 Mammalian |
| 21 | 27 | 100.0 | 5 | ADR3771 | Adr3771 Human mag |
| 22 | 27 | 100.0 | 6 | AAAP0519 | Aap0519 Sequence |
| 23 | 27 | 100.0 | 6 | AP50694 | Ap50694 Sequence |
| 24 | 27 | 100.0 | 6 | AAAP0632 | Aap0632 Substance |
| 25 | 27 | 100.0 | 6 | AAP61486 | Aap61486 Peptide h |

26 27 100.0 6 2 AAR07893 Har07893 Cyclocopt
 27 27 100.0 6 2 AAR21959 Har21959 Substance
 28 27 100.0 6 2 AAR27694 Har27694 Cyclic ta
 29 27 100.0 6 2 AAR99686 Har99686 Substance
 30 27 100.0 6 2 AAW2706 Harw2706 Human tac
 31 27 100.0 6 2 AAW2659 Harw2659 Human tac
 32 27 100.0 6 3 AAY67575 Hay67575 P antago
 33 27 100.0 6 4 AAB82453 Har82453 Fluorinat
 34 27 100.0 6 4 AAB82436 Har82436 Fluorinat
 35 27 100.0 6 4 AAB91121 Har91121 Tachykini
 36 27 100.0 6 4 AAB91425 Har91425 Tachykini
 37 27 100.0 6 4 AAB91419 Har91419 Tachykini
 38 27 100.0 6 4 AAG99351 Hay99351 Atypical
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 40 27 100.0 6 5 ABB10085 Harb10085 Substance
 41 27 100.0 6 4 AAB91420 Har91420 High acti
 42 27 100.0 6 4 AAB94202 Har94202 High acti
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 46 27 100.0 7 2 AAB92662 Har92662 Human tac
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 81 27 100.0 10 2 AAY06939 Hay06939 Substance
 82 27 100.0 10 2 AAM92663 Harw92663 Human tac
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 84 27 100.0 10 4 ARG99347 Har99347 Atypical
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| RESULT 1 | | | |
| C | ARJ3009 | D | ARJ3009 standard; peptide; 5 AA. |
| X | AAR21970 | X | AAR21970 |
| T | 25-MAR-2003 (revised) | T | 25-MAR-2003 (revised) |
| X | 02-APR-1993 (first entry) | X | 02-APR-1993 (first entry) |
| Alpha-substituted short peptide. | | | |
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ALIGNMENTS

| | | |
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| FT | Key | Location/Qualifiers |
| FT | Modified-site | 4 |
| /note= | "alpha-Me-Leu" | |
| FT | Modified-site | 5 |
| /note= | "Met-NH2" | |
| XX | XX | WO219254-A1. |
| XX | XX | PD 12-NOV-1992. |
| XX | XX | PR 15-APR-1992; 92W0-US093119. |
| XX | XX | PR 24-APR-1991; 91US-00690755. |
| XX | XX | PR 20-MAR-1992; 92US-00652086. |
| PA | PA | (WARN) WARNER LAMBERT CO. |
| XX | XX | PI Horwell DC, Hughes J, Richardson RS, Howson W; |
| XX | XX | DR WPI; 1992-39852/48. |
| XX | CC | New alpha-subsed. polypeptide are e.g. selective receptor ligands - for treating inflammation, pain, stroke, ulcers, hypertension, heart failure, depression, cancer, asthma, psychosis, arthritis, etc. |
| CC | CC | Claim 3; Page 41; 46pp; English. |
| CC | CC | The peptide is a specifically claimed example of a group of generically claimed mono-, di-, tri-, tetra- and penta-peptides which include a substituent on an alpha-C atom in the chain. Such substitution may modify the bioavailability, stability or absorbability of the peptide and hence may improve the activity of the peptide as a drug. Depending on the nature of the parent peptide (hormone, endorphin, CCK, NK2, chemotactic peptide, etc.), the modified peptides are variously useful for treating obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation, addictive drug withdrawal symptoms, hypertension, heart, failure, cognition or memory disorders, spasticity, depression, diabetes, cancer, asthma, bladder dysfunction, psychosis and arthritis; and as contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct Pb field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.) |
| Oy | Oy | Sequence 5 AA; |
| Db | Db | Query Match ID AAR33008 Best Local Similarity 100.0%; Score 27; DB 2; Length 5; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 FRGLM 5 Db 1 FRGLM 5 |
| RESULT 2 | | |
| XX | XX | AAR33008 standard; peptide; 5 AA. |
| XX | XX | AAR33008; |
| DT | DT | 25-MAR-2003 (revised) |
| DT | DT | 02-APR-1993 (first entry) |
| XX | XX | Alpha-substituted short peptide. |
| DB | DB | Alpha-substituted short peptide. |
| OS | OS | Synthetic. |
| XX | XX | CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia; improved bioavailability. |
| FF | Key | Location/Qualifiers |
| FT | Modified-site | 2 |
| FT | Modified-site | /note= "alpha-Me-Phe" |
| FT | Modified-site | 5 |

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

On protein - protein search, using sw model
Run on: October 26, 2005, 08:12:17 ; Search time 124.444 seconds
Sequence: perfect score: 27/27

Title: US-10-053-669-1.rup
Post-processing: Minimum DB seq length: 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 3223

Minimum DB seq length: 0
Post-processing: Maximum Match 0%
Listing first 150 summaries

Database : UniProt-03+
1: uniprot_sprot:
2: uniprot_trembl:
3: Trembl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB | ID | Description |
|------------|-------|-------|--------------|----|------------|-----------------------------|
| 1 | 27 | 100.0 | 11 | 1 | TKN4_PSEGU | Pseudophryne pseudephryne |
| 2 | 27 | 100.0 | 11 | 1 | TKN5_PSEGU | Pseudophryne pseudephryne |
| 3 | 27 | 100.0 | 11 | 1 | TKNA_CAVPO | Cavia porcellus |
| 4 | 27 | 100.0 | 11 | 1 | TKNA_CHICK | Gallus gallus |
| 5 | 27 | 100.0 | 11 | 1 | TKNA_HORSE | Equus caballus |
| 6 | 27 | 100.0 | 11 | 1 | TKNA_ONCMI | Oncorhynchus mykiss |
| 7 | 27 | 100.0 | 11 | 1 | TKNA_SCYCA | Scylliorhinus scylliorhinus |
| 8 | 24 | 88.9 | 10 | 1 | TKN1_SCYCA | Scylliorhinus scylliorhinus |
| 9 | 24 | 88.9 | 10 | 1 | TKNB_RANCA | Rana catesbeiana |
| 10 | 24 | 88.9 | 10 | 1 | TKNS_AEDAE | Aedes aegypti |
| 11 | 24 | 88.9 | 10 | 1 | TKS2_AEDAE | Aedes aegypti |
| 12 | 24 | 88.9 | 11 | 1 | TKN1_UPEIN | Upoleia rufa |
| 13 | 24 | 88.9 | 11 | 1 | TKN1_UPERU | Upoleia rufa |
| 14 | 24 | 88.9 | 11 | 1 | TKN2_UPERU | Upoleia rufa |
| 15 | 24 | 88.9 | 11 | 1 | TKNA_RANCA | Rana catesbeiana |
| 16 | 24 | 88.9 | 11 | 1 | TKNA_RANRI | Rana ridibunda |
| 17 | 24 | 88.9 | 11 | 1 | TKN1_PHYFU | Physalaemus fischeri |
| 18 | 24 | 88.9 | 11 | 2 | QD9R8 | Aedes aegypti |
| 19 | 21 | 77.8 | 10 | 1 | TKNB_RANRI | Rana ridibunda |
| 20 | 21 | 77.8 | 10 | 1 | TKNC_RANCA | Rana catesbeiana |
| 21 | 21 | 77.8 | 10 | 1 | TKN1_PHYBI | Phyllobius pomaceus |
| 22 | 21 | 77.8 | 10 | 2 | Q76M8 | Eurypharinx poeciloptera |
| 23 | 21 | 77.8 | 11 | 1 | TKNA_GADMO | Gadomia mormona |
| 24 | 21 | 77.8 | 11 | 1 | TKN1_ELECT | Eleotris electra |
| 25 | 21 | 77.8 | 11 | 1 | TKN1_ELEMO | Eleotris elongatus |
| 26 | 20 | 74.1 | 10 | 1 | TKNB_CHICK | Gallus gallus |
| 27 | 20 | 74.1 | 10 | 1 | TKN1_ONCMI | Oncorhynchus mykiss |
| 28 | 20 | 74.1 | 10 | 1 | TKN1_PIG | Sus scrofa |
| 29 | 20 | 74.1 | 10 | 1 | TKN1_RANRI | Rana ridibunda |
| 30 | 20 | 74.1 | 10 | 1 | TKP6_LEUMA | Leucophæa leucophæa |
| 31 | 20 | 74.1 | 10 | 1 | TRP7_LEUMA | Leucophæa leucophæa |
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| 105 | 12 | 44.4 | 8 | 1 | CCCN-MACEU | P68126 | macropus eu | CC | -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and contract (directly or indirectly) many smooth muscles. |
| 106 | 12 | 44.4 | 8 | 1 | DYSS-LIMIN | P82079 | limnodynast | CC | -!- SUBCELLULAR LOCATION: Secreted. |
| 107 | 12 | 44.4 | 8 | 2 | O13591 | O13591 | saccharomyces | CC | -!- TISSUE SPECIFICITY: Skin. |
| 108 | 12 | 44.4 | 8 | 2 | OP0K3 | OP0k3 | homo sapien | CC | -!- SIMILARITY: Belongs to the tachykinin family. |
| 109 | 12 | 44.4 | 8 | 2 | Q5RQ8 | Q5i4q8 | bubalus bub | CC | -!- FUNCTION: Belongs to the tachykinin family. |
| 110 | 12 | 44.4 | 8 | 2 | Q9T4V2 | Q9T4V2 | asterina pe | CC | -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and contract (directly or indirectly) many smooth muscles. |
| 111 | 12 | 44.4 | 8 | 2 | Q9T002 | Q9T002 | terratoras | DR | -!- SIMILARITY: Belongs to the tachykinin family. |
| 112 | 12 | 44.4 | 8 | 2 | Q7X139 | Q7x139 | staphylococ | DR | -!- FUNCTION: Belongs to the tachykinin family. |
| 113 | 12 | 44.4 | 8 | 2 | Q7X145 | Q7x145 | staphylococ | DR | -!- SIMILARITY: Belongs to the tachykinin family. |
| 114 | 12 | 44.4 | 8 | 2 | Q7Z0J1 | Q7z0j1 | homo sapien | DR | -!- SUBCELLULAR LOCATION: Secreted. |
| 115 | 12 | 44.4 | 9 | 1 | F1BB-ERYPA | P19346 | erythrocyte | DR | -!- TISSUE SPECIFICITY: Skin. |
| 116 | 12 | 44.4 | 9 | 1 | F1BB-THEGE | P19342 | theropithec | DR | -!- SIMILARITY: Belongs to the tachykinin family. |
| 117 | 12 | 44.4 | 9 | 1 | RE42-LITR0 | P82075 | litoria rub | DR | -!- FUNCTION: Tachykinin; 1. |
| 118 | 12 | 44.4 | 9 | 2 | Q9K887 | Q9K887 | homo sapien | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 119 | 12 | 44.4 | 9 | 2 | Q7RBU6 | Q7rbu6 | plasmodium | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 120 | 12 | 44.4 | 9 | 2 | Q8M0N1 | Q8m0n1 | cebus apella | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 121 | 12 | 44.4 | 9 | 2 | Q8M0N2 | Q8m0n2 | callithrix jacchus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 122 | 12 | 44.4 | 9 | 2 | Q8M0N3 | Q8m0n3 | cebus apella | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 123 | 12 | 44.4 | 9 | 2 | Q8M0N4 | Q8m0n4 | leontopithecus rosalia | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 124 | 12 | 44.4 | 9 | 2 | Q8M0N5 | Q8m0n5 | aguinus fu | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 125 | 12 | 44.4 | 9 | 2 | Q8M0N6 | Q8m0n6 | aotus azarae | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 126 | 12 | 44.4 | 9 | 2 | Q8M0N7 | Q8m0n7 | saimiri sciureus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 127 | 12 | 44.4 | 9 | 2 | Q8M0N8 | Q8m0n8 | cebus apella | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 128 | 12 | 44.4 | 9 | 2 | Q8M0N9 | Q8m0n9 | callicebus personatus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 129 | 12 | 44.4 | 9 | 2 | Q8M0T7 | Q8m0t7 | eulemur fulvus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 130 | 12 | 44.4 | 9 | 2 | Q8M0T8 | Q8m0t8 | euothrius fulvus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 131 | 12 | 44.4 | 9 | 2 | Q7M394 | Q7m394 | sub scrofa | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 132 | 12 | 44.4 | 9 | 2 | Q691D6 | Q691d6 | anolis sagrei | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 133 | 12 | 44.4 | 9 | 2 | Q6XBN2 | Q6xbn2 | vittia pacifica | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 134 | 12 | 44.4 | 9 | 2 | Q8G996 | Q8g996 | pyrrhocorax graculus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 135 | 12 | 44.4 | 9 | 2 | Q9GJ36 | Q9gj36 | juncus effusus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 136 | 12 | 44.4 | 9 | 2 | Q9MMF4 | Q9mmf4 | buteo rufinus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 137 | 12 | 44.4 | 9 | 2 | Q9PKG9 | Q9pkg9 | buteo buteo | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 138 | 12 | 44.4 | 9 | 2 | Q9TE88 | Q9te88 | gecko gecko | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 139 | 12 | 44.4 | 9 | 2 | P82440 | P82440 | nicotiana tabacum | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 140 | 12 | 44.4 | 9 | 2 | Q9AXH8 | Q9axh8 | mesembryanthemum crystallinum | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 141 | 12 | 44.4 | 9 | 2 | Q7M139 | Q7m139 | unidentified | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 142 | 12 | 44.4 | 9 | 2 | Q6YF34 | Q6yf34 | rattus norvegicus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 143 | 12 | 44.4 | 9 | 2 | Q7LUH0 | Q7luh0 | oquiubo | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 144 | 12 | 44.4 | 9 | 2 | Q6T1E2 | Q6t1e2 | sars corona | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 145 | 12 | 44.4 | 9 | 2 | Q7L2T5 | Q7l2t5 | rana esculenta | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 146 | 12 | 44.4 | 9 | 2 | Q7Z0J9 | Q7z0j9 | ozioppi human immunodeficiency virus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 147 | 12 | 44.4 | 9 | 2 | Q7Z2J3 | Q7z2j3 | human immunodeficiency virus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 148 | 12 | 44.4 | 9 | 2 | Q7ZPJ5 | Q7zpj5 | human immunodeficiency virus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 149 | 12 | 44.4 | 9 | 2 | Q7ZPJ7 | Q7zpj7 | human immunodeficiency virus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |
| 150 | 12 | 44.4 | 9 | 2 | Q7ZPK1 | Q7zpk1 | human immunodeficiency virus | DR | -!- PROSTIM; P800267; TACHYKININ; 1. |

ALIGNMENTS

| RESULT | 1 | TRN4_PSEGU | STANDARD; | PRT; | 11 AA. | TKNS_PSEGU | STANDARD; | PRT; | 11 AA. | |
|------------|----|------------|-----------|------|--------------------------------|---|-----------|------|--|---|
| DTN4_PSEGU | DT | AC | PR2989; | DT | 01-NOV-1995 (Rel. 32, Created) | AC | P42930; | DT | 01-NOV-1995 (Rel. 32, Created) | |
| | | | | | DT | 01-NOV-1995 (Rel. 32, Last sequence update) | | | DT | 01-NOV-1995 (Rel. 32, Last sequence update) |
| | | | | | DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | DE | Substance P-like peptide II (PG-SPII). |
| | | | | | | | | | OS | Pseudophryne guntheri (Guenther's toadlet). |
| | | | | | | | | | OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae; Myobatrachinae; Pseudophryne. |
| | | | | | | | | | OC | "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri." |
| | | | | | | | | | RT | Peptides 11:299-304 (1990). |
| | | | | | | | | | SEQUENCE | TISSUE=skin secretion; |
| | | | | | | | | | RX | MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K; |
| | | | | | | | | | RA | Simmaco M., Severini C., de Blase D., Barra F., |
| | | | | | | | | | RA | Roberts J.D., Melchiorri P., Braspamer V.; |
| | | | | | | | | | RT | "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri." |
| | | | | | | | | | SEQUENCE | 11 AA; |
| | | | | | | | | | RL | RT |
| | | | | | | | | | CC | -!- SUBCELLULAR LOCATION: Secreted. |
| | | | | | | | | | CC | -!- TISSUE SPECIFICITY: Skin. |
| | | | | | | | | | CC | -!- SIMILARITY: Belongs to the tachykinin family. |
| | | | | | | | | | DR | DR |
| | | | | | | | | | DR | INTERPRO; IPR008215; Tachykinin. |
| | | | | | | | | | DR | INTERPRO; IPR00202; Tachykinin. |
| | | | | | | | | | DR | Pfam; PF02202; Tachykinin. |
| | | | | | | | | | DR | PROSITE; PS00267; TACHYKININ; 1. |
| | | | | | | | | | DR | AMIDATION; Amphibian defense peptide; Direct protein sequencing; |
| | | | | | | | | | DR | Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin. |
| | | | | | | | | | FT | MOD_RES 1 1 Pyrrolidone carboxylic acid. |
| | | | | | | | | | FT | MOD_RES 11 1 Methionine amide. |
| | | | | | | | | | SQ | SEQUENCE 11 AA; 1293 MW; 3A247C2CCB1457 CRC64; |
| | | | | | | | | | Query Match 100%; Score 27; DB 1; Length 11; | |
| | | | | | | | | | Best Local Similarity 100%; Pred. No. 30; | |
| | | | | | | | | | Matches 5; Conservative 0; Mismatches 0; | |
| | | | | | | | | | Indels 0; Gaps 0; | |
| | | | | | | | | | RT | |
| | | | | | | | | | SEQUENCE 11 AA; | |
| | | | | | | | | | RL | |

RESULT 1
 TRN4_PSEGU STANDARD; PRT; 11 AA.
 ID TRN4_PSEGU DT 01-NOV-1995 (Rel. 32, Last sequence update)
 AC PR2989; DT 05-JUL-2004 (Rel. 44, Last annotation update)
 CC OS Substance P-like Peptide I (PG-SPI).
 OC Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Butelostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae; Myobatrachinae; Pseudophryne.
 OC RN [1] Peptide Sequence.
 OC RC TISSUE-Skin secretion'; MEDLINE=90287814; PubMed=2356157; DOI=10.1016/0196-9781(90)90086-K;
 RA RA Simmaco M., Severini C., de Blase D., Barra F.,
 RA Roberta J.D., Melchiorri P., Braspamer V.;
 RA RT 'Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.'; Peptides 11:299-304 (1990).
 RN [1]

| | | Matches | 5; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|--|----|---------|--------------|--------------|------------|------------|--------|--------|------|------|----|
| 20alpha-hydroxyoctapeptide Fmri | | | | | | | | | | | |
| neuropeptide Fmri | OY | 1 | FRGLM | 5 | | | | | | | |
| Met-enkephalin - b | Db | 7 | FRGLM | 11 | | | | | | | |
| Met-enkephalin-Arg | | | | | | | | | | | |
| telomeric and tetr | | | | | | | | | | | |
| fibrinopeptide B - | | | | | | | | | | | |
| transaldolase (EC | | | | | | | | | | | |
| neuropeptide Grb-A | | | | | | | | | | | |
| callifERFamide 13 | | | | | | | | | | | |
| bone g1a protein - | | | | | | | | | | | |
| leucosulfatfakinin II | | | | | | | | | | | |
| leucosulfatfakinin II | | | | | | | | | | | |
| transfelin - sheep | | | | | | | | | | | |
| perisulfatfakinin - A | | | | | | | | | | | |
| rannatachykinin D - | | | | | | | | | | | |
| Ig heavy chain CRD | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| 27.5 kDa structure | | | | | | | | | | | |
| 27.5K structural p | | | | | | | | | | | |
| 27.5K structural p | | | | | | | | | | | |
| 28.5K structural P | | | | | | | | | | | |
| collagen alpha 1(I) | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| Ig heavy chain CRD | | | | | | | | | | | |
| aspartate transam | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| NADH dehydrogenas | | | | | | | | | | | |
| Globulin IV alpha | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| trichodectein I - | | | | | | | | | | | |
| trichodectein II - | | | | | | | | | | | |
| protein QA300040 - | | | | | | | | | | | |
| polygalacturonase | | | | | | | | | | | |
| Ig gamma chain C ϵ | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
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| T-cell receptor be | | | | | | | | | | | |
| T-cell receptor be | | | | | | | | | | | |
| R γ 1 Pept. 20, 171-180, 1988 | | | | | | | | | | | |
| A β -Title: Larg3 substance P and neurokinin A from chicken small intestine. | | | | | | | | | | | |
| A β -Reference number: JN0023; MUID:88204263; PMID:2452461 | | | | | | | | | | | |
| A β -Accession: JN0023 | | | | | | | | | | | |
| A β -Molecule type: protein | | | | | | | | | | | |
| A β -Residues: 1-11 <CON> | | | | | | | | | | | |
| A β -Cross-references: UNIPROT:P19850 | | | | | | | | | | | |
| C β -Superfamily: Substance P precursor | | | | | | | | | | | |
| C β -Keywords: amidated carboxyl end; tachykinin | | | | | | | | | | | |
| C β -Modified site: amidated carboxyl end (Met) #status predicted | | | | | | | | | | | |
| Query Match | | 100.0% | | Score 27; | DB 2; | Length 11; | | | | | |
| Best Local Similarity | | 100.0% | | Pred. No. 3; | | | | | | | |
| Matches | | 5; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; | |
| OY | | 1 | FRGLM | 5 | | | | | | | |
| Db | | 7 | FRGLM | 11 | | | | | | | |

RESULT 1

A β -Title: Primary amino acid sequence of guinea-pig substance P.
A β -Reference number: A60654; MUID:9044685; PMID:2478925
A β -Accession: A60654
A β -Molecule type: protein
A β -Residues: 1-11 <MUR>
A β -Cross-reference: UNIPROT:P01290
C β -Family: substance P precursor
C β -Keywords: amidated carboxyl end; neuropeptide; tachykinin
C β -Modified site: amidated carboxyl end (Met) #status experimental

Query March 100.0% Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;

ALIGNMENTS

RESULT 4

S33300 probable substance P - smaller spotted catshark
C β -Species: Scylliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C β -Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C β -Accession: S33300
R Waugh, D.; Wang, Y.; Razon, N.; Balment, R.J.; Conlon, J.M.
Bur. J. Biochem. 214, 460-474, 1993
A β -Title: Primary structures and biological activities of substance-P-related peptides from
A β -Reference number: S33300; MUID:93292508; PMID:685693
A β -Molecule type: protein

RESULT 2

SPHO substance P - horse

C β -Species: Equus caballus (domestic horse)
C β -Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C β -Accession: A01558
R Studer, R.O.; Tzeciaik, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A β -Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
A β -Reference number: A01558
A β -Accession: A01558
A β -Molecule type: protein
A β -Residues: 1-11 <SRY>
A β -Cross-references: UNIPROT:P01290
C β -Superfamily: Substance P precursor
C β -Keywords: amidated carboxyl end; hormone
P β -Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 27; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRGLM 5
Db 7 FRGLM 11

RESULT 3

JN0023 substance P - chicken

C β -Species: Gallus gallus (chicken)
C β -Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C β -Accession: JN0023
R Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A β -Title: Larg3 substance P and neurokinin A from chicken small intestine.
A β -Reference number: JN0023; MUID:88204263; PMID:2452461
A β -Accession: JN0023
A β -Molecule type: protein
A β -Residues: 1-11 <CON>
A β -Cross-references: UNIPROT:P19850
C β -Superfamily: Substance P precursor
C β -Keywords: amidated carboxyl end; tachykinin
C β -Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FRGLM 5
Db 7 FRGLM 11

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Om protein - protein search, using SW model

Run on: October 26, 2005, 08:13:37 ; Search time 120.556 seconds
(w/o alignments)
17.316 Million cell updates/sec

Title: USP10-053-669-1.rabp
Perfect score: 27
Sequence: USPFGIMV-5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database : ~~Unpublished applications AA~~
1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep:
2: /cgn2_6/ptodata/1/pubaa/PCTC_NEWPUB.pep:
3: /cgn2_6/ptodata/1/pubaa/US06_NEWPUB.pep:
4: /cgn2_6/ptodata/1/pubaa/US05_PUBCOMB.pep:
5: /cgn2_6/ptodata/1/pubaa/US07_NEWPUB.pep:
6: /cgn2_6/ptodata/1/pubaa/PCRTUS_PUBCOMB.pep:
7: /cgn2_6/ptodata/1/pubaa/US08_NEWPUB.pep:
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9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep:
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12: /cgn2_6/ptodata/1/pubaa/US09_NEWPUB.pep:
13: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep:
14: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep:
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep:
16: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep:
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18: /cgn2_6/ptodata/1/pubaa/US11A_PUBCOMB.pep:
19: /cgn2_6/ptodata/1/pubaa/US11A_NEWPUB.pep:
20: /cgn2_6/ptodata/1/pubaa/US11_NEWPUB.pep:
21: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:
22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result NO. | Score | Query | Match Length | DB ID | Description |
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| 1 | 27 | 100.0 | 5 | 9 US-09-265-690C-1 | Sequence 1, Appli |
| 2 | 27 | 100.0 | 5 | 14 US-10-053-661-1 | Sequence 1, Appli |
| 3 | 27 | 100.0 | 5 | 15 US-10-124-187-3 | Sequence 3, Appli |
| 4 | 27 | 100.0 | 5 | 16 US-10-658-741-3 | Sequence 3, Appli |
| 5 | 27 | 100.0 | 5 | 16 US-10-805-881-1 | Sequence 1, Appli |
| 6 | 27 | 100.0 | 5 | 16 US-10-720-309-3 | Sequence 3, Appli |
| 7 | 27 | 100.0 | 5 | 17 US-10-497-621-15 | Sequence 15, Appli |
| 8 | 27 | 100.0 | 5 | 20 US-11-056-697-604 | Sequence 604, Appli |
| 9 | 27 | 100.0 | 5 | 20 US-11-025-5494-3 | Sequence 3, Appli |
| 10 | 27 | 100.0 | 6 | 14 US-10-168-789A-38 | Sequence 38, Appli |
| 11 | 27 | 100.0 | 6 | 17 US-11-066-697-625 | Sequence 14, Appli |
| 12 | 27 | 100.0 | 6 | 20 US-11-066-697-595 | Sequence 595, App |
| 13 | 27 | 100.0 | 6 | 20 US-11-066-697-597 | Sequence 597, App |
| 14 | 27 | 100.0 | 6 | 20 US-11-066-697-601 | Sequence 601, App |
| 15 | 27 | 100.0 | 7 | 14 US-10-036-542-110 | Sequence 110, App |
| 16 | 27 | 100.0 | 7 | 14 US-10-134-187-2 | Sequence 111, App |
| 17 | 27 | 100.0 | 7 | 14 US-10-168-789A-37 | Sequence 37, App |
| 18 | 27 | 100.0 | 7 | 15 US-10-134-187-2 | Sequence 2, Appli |
| 19 | 27 | 100.0 | 7 | 16 US-10-688-781-2 | Sequence 2, Appli |
| 20 | 27 | 100.0 | 7 | 16 US-10-720-039-2 | Sequence 2, Appli |
| 21 | 27 | 100.0 | 7 | 17 US-10-497-628-13 | Sequence 13, Appli |
| 22 | 27 | 100.0 | 7 | 20 US-11-066-697-596 | Sequence 596, App |
| 23 | 27 | 100.0 | 7 | 20 US-11-066-697-607 | Sequence 607, App |
| 24 | 27 | 100.0 | 7 | 20 US-11-025-494-2 | Sequence 2, Appli |
| 25 | 27 | 100.0 | 8 | 14 US-10-168-789A-36 | Sequence 36, Appli |
| 26 | 27 | 100.0 | 8 | 15 US-10-497-628-12 | Sequence 12, Appli |
| 27 | 27 | 100.0 | 8 | 20 US-11-066-697-583 | Sequence 583, App |
| 28 | 27 | 100.0 | 8 | 20 US-11-066-697-592 | Sequence 592, App |
| 29 | 27 | 100.0 | 8 | 20 US-11-066-697-600 | Sequence 600, App |
| 30 | 27 | 100.0 | 9 | 14 US-10-016-542-112 | Sequence 112, App |
| 31 | 27 | 100.0 | 9 | 14 US-10-168-789A-35 | Sequence 35, Appli |
| 32 | 27 | 100.0 | 9 | 15 US-10-134-187-1 | Sequence 1, Appli |
| 33 | 27 | 100.0 | 9 | 16 US-10-688-741-1 | Sequence 1, Appli |
| 34 | 27 | 100.0 | 9 | 16 US-10-720-039-1 | Sequence 1, Appli |
| 35 | 27 | 100.0 | 9 | 16 US-11-066-697-545 | Sequence 545, App |
| 36 | 27 | 100.0 | 9 | 20 US-11-066-697-622 | Sequence 622, App |
| 37 | 27 | 100.0 | 9 | 20 US-11-025-494-1 | Sequence 1, Appli |
| 38 | 27 | 100.0 | 10 | 17 US-10-451-304-1 | Sequence 1, Appli |
| 39 | 27 | 100.0 | 10 | 20 US-11-066-697-621 | Sequence 1, Appli |
| 40 | 27 | 100.0 | 10 | 20 US-11-079-477-621 | Sequence 1, Appli |
| 41 | 27 | 100.0 | 10 | 20 US-11-079-477-621 | Sequence 1, Appli |
| 42 | 27 | 100.0 | 11 | 9 US-09-265-690C-3 | Sequence 3, Appli |
| 43 | 27 | 100.0 | 11 | 9 US-09-988-792-10 | Sequence 64, Appli |
| 44 | 27 | 100.0 | 11 | 9 US-09-981-0918-26 | Sequence 26, Appli |
| 45 | 27 | 100.0 | 11 | 10 US-09-988-792-1 | Sequence 1, Appli |
| 46 | 27 | 100.0 | 11 | 10 US-09-988-792-6 | Sequence 6, Appli |
| 47 | 27 | 100.0 | 11 | 10 US-09-988-792-7 | Sequence 7, Appli |
| 48 | 27 | 100.0 | 11 | 10 US-09-988-792-8 | Sequence 8, Appli |
| 49 | 27 | 100.0 | 11 | 11 US-09-988-792-10 | Sequence 10, Appli |
| 50 | 27 | 100.0 | 11 | 13 US-10-002-593-4 | Sequence 4, Appli |
| 51 | 27 | 100.0 | 11 | 14 US-10-230-133-1 | Sequence 1, Appli |
| 52 | 27 | 100.0 | 11 | 14 US-10-053-669-3 | Sequence 3, Appli |
| 53 | 27 | 100.0 | 11 | 14 US-10-211-994-3 | Sequence 3, Appli |
| 54 | 27 | 100.0 | 11 | 14 US-10-114-823B-24 | Sequence 24, Appli |
| 55 | 27 | 100.0 | 11 | 14 US-10-197-954-130 | Sequence 130, App |
| 56 | 27 | 100.0 | 11 | 14 US-10-251-703-25 | Sequence 25, Appli |
| 57 | 27 | 100.0 | 11 | 14 US-10-168-789A-17 | Sequence 17, Appli |
| 58 | 27 | 100.0 | 11 | 14 US-10-423-714-4 | Sequence 4, Appli |
| 59 | 27 | 100.0 | 11 | 15 US-10-54-554-27 | Sequence 27, Appli |
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| 61 | 27 | 100.0 | 11 | 15 US-10-197-954-130 | Sequence 130, App |
| 62 | 27 | 100.0 | 11 | 15 US-10-289-009-25 | Sequence 25, Appli |
| 63 | 27 | 100.0 | 11 | 15 US-10-289-009-26 | Sequence 26, Appli |
| 64 | 27 | 100.0 | 11 | 15 US-10-167-627-55 | Sequence 65, Appli |
| 65 | 27 | 100.0 | 11 | 16 US-10-695-536-1 | Sequence 1, Appli |
| 66 | 27 | 100.0 | 11 | 16 US-10-805-891-3 | Sequence 3, Appli |
| 67 | 27 | 100.0 | 11 | 17 US-10-813-056-4 | Sequence 4, Appli |
| 68 | 27 | 100.0 | 11 | 17 US-10-160-005-130 | Sequence 130, App |
| 69 | 27 | 100.0 | 11 | 17 US-10-839-017-13 | Sequence 13, Appli |
| 70 | 27 | 100.0 | 11 | 17 US-10-768-974-1 | Sequence 1, Appli |
| 71 | 27 | 100.0 | 11 | 17 US-10-854-646-1 | Sequence 1, Appli |
| 72 | 27 | 100.0 | 11 | 17 US-10-854-646-5 | Sequence 5, Appli |
| 73 | 27 | 100.0 | 11 | 17 US-10-854-646-10 | Sequence 6, Appli |
| 74 | 27 | 100.0 | 11 | 17 US-10-854-646-13 | Sequence 10, Appli |
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| 78 | 27 | 100.0 | 11 | 20 US-11-021-951-164 | Sequence 24, Appli |
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| 80 | 27 | 100.0 | 11 | 20 US-11-066-697-578 | Sequence 4, Appli |
| 81 | 27 | 100.0 | 11 | 20 US-11-066-697-612 | Sequence 578, Appli |
| 82 | 27 | 100.0 | 11 | 20 US-11-066-697-614 | Sequence 612, Appli |
| 83 | 27 | 100.0 | 11 | 20 US-11-066-697-625 | Sequence 614, Appli |
| 84 | 27 | 100.0 | 11 | 20 US-11-066-697-626 | Sequence 625, Appli |
| 85 | 27 | 100.0 | 11 | 20 US-11-066-697-626 | Sequence 626, Appli |

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. Score Query Match Length DB ID Description

RESULT 1
US-09-265-690C-1

ALIGNMENTS

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85      24      88.9      5    17 US-10-497-638-16
86      24      88.9      5    10 US-09-988-722-11
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89      24      88.9      10   15 US-10-445-400-1
90      24      88.9      10   15 US-10-445-400-2
91      24      88.9      10   18 US-10-994-170-1
92      24      88.9      10   18 US-10-994-170-2
93      24      88.9      11   14 US-10-197-952-117
94      24      88.9      11   14 US-10-197-954-138
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97      24      88.9      11   20 US-11-066-697-562
98      24      88.9      11   20 US-11-131-034-82
99      22      81.5      4    17 US-10-821-240A-270
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101     22      81.5      7    17 US-10-938-29-82
102     22      81.5      7    17 US-10-754-341-15
103     22      81.5      7    20 US-11-131-034-82
104     22      81.5      7    20 US-11-131-034-82
105     22      81.5      8    17 US-10-938-29-83
106     22      81.5      8    17 US-10-931-627-21
107     22      81.5      8    18 US-10-753-181-70
108     22      81.5      8    20 US-11-131-034-83
109     22      81.5      8    20 US-11-131-034-83
110     22      81.5      9    19 US-09-835-948-34
111     22      81.5      9    19 US-09-835-948-52
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115     22      81.5      9    19 US-09-835-948-173
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121     22      81.5      9    14 US-10-172-597-52
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125     22      81.5      9    14 US-10-172-597-173
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Sequence 1, Application US/09265590C
Publication No. US20010051345A1
GENERAL INFORMATION:
APPLICANT: Wells, Bert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Macromolecules
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265, 690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 1
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: 5
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: AMIDATION
US-09-265-690C-1

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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
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RESULT 2
US-10-053-669-1

Sequence 1, Application US/10053669
Publication No. US20030077658A1
GENERAL INFORMATION:
APPLICANT: Wells, Bert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Macromolecules
FILE REFERENCE: NI27-005
CURRENT APPLICATION NUMBER: US/10/053, 669
CURRENT FILING DATE: 2002-01-24
PRIORITY APPLICATION NUMBER: 09/265, 690
PRIORITY FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 1
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: 5
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: AMIDATION
US-10-053-669-1

Query Match 100.0%; Score 27; DB 14; Length 5;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-10-134-187-3

Sequence 3, Application US/10134187
Publication No. US20030202981A1
GENERAL INFORMATION:
APPLICANT: Kream, Richard M.
APPLICANT: Kream, Richard M.
APPLICANT: Kream, Richard M.
TITLE OF INVENTION: Chimeric Hybrid Analgesics

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GenCore version 5.1.6

Om protein - protein search, using SW model
Run on: October 26, 2005, 08:17:28 ; Search time 33,889 seconds
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11.014 Million cell updates/sec

Title: US-10-053-669-1
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 60 | 27 | 100.0 | 11 | 3 | US-08-890-15A-4 | |
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| 82 | 24 | 88.9 | 11 | 2 | US-08-796-598-7 | |
| 83 | 24 | 88.9 | 11 | 2 | US-08-447-175A-7 | |
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| 85 | 24 | 88.9 | 11 | 2 | US-07-737-371E-37 | |
| 86 | 24 | 88.9 | 11 | 3 | US-09-214-611-1 | |
| 87 | 22 | 81.5 | 5 | 2 | US-07-737-371E-47 | |
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| 90 | 22 | 81.5 | 9 | 3 | US-09-492-543-34 | |
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| 100 | 22 | 81.5 | 11 | 2 | US-07-737-371E-14 | |

ALIGNMENTS

RESULT 1
US-07-934-553-2
Sequence 2, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALCON, LUNGMIUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: TILTON, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: October 26, 2005, 08:08:06 ; Search time 133.333 Seconds
(without alignments)
14.504 Million cell updates/sec

Title: <US31020593669>=1
Perfect score: 27

Sequence: 1 FFGLM 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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5: geneseq2002a:*

6: geneseq2002ab:*

7: geneseq2003b:*

8: geneseq2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 19 | 27 | 100.0 | 5 7 | ADF2530 Substance |
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| 126 | 27 | 100.0 | 11 | 2 | AAW92681 | harr92681 Human tac |
| 127 | 27 | 100.0 | 11 | 2 | AAW2672 | harr2672 Human tac |
| 128 | 27 | 100.0 | 11 | 2 | AAW2690 | harr2690 Human tac |
| 129 | 27 | 100.0 | 11 | 2 | AAY30985 | harry30985 Non-cross |
| 130 | 27 | 100.0 | 11 | 2 | AAY03156 | harry03156 Substance |
| 131 | 27 | 100.0 | 11 | 2 | AD124903 | adi124903 Substance |
| 132 | 27 | 100.0 | 11 | 2 | AAW23027 | harr23027 Human/rat |
| 133 | 27 | 100.0 | 11 | 3 | AAH18483 | harr18483 Peptide # |
| 134 | 27 | 100.0 | 11 | 3 | AAV32382 | Cell diff |
| 135 | 27 | 100.0 | 11 | 3 | AAH06260 | harr06260 Substance |
| 136 | 27 | 100.0 | 11 | 3 | AAH08614 | harr08614 Peptidase |
| 137 | 27 | 100.0 | 11 | 4 | AAH03111 | harr0311 Peptidase |
| 138 | 27 | 100.0 | 11 | 4 | AAH50312 | harr50312 Peptidase |
| 139 | 27 | 100.0 | 11 | 4 | AAH0306 | harr0306 Substance |
| 140 | 27 | 100.0 | 11 | 4 | AAH0316 | harr0316 Peptidase |
| 141 | 27 | 100.0 | 11 | 4 | AAH50544 | harr50544 Prolyl en |
| 142 | 27 | 100.0 | 11 | 4 | AAH91450 | harr91450 Tachykinin |
| 143 | 27 | 100.0 | 11 | 4 | AAH91438 | harr91438 Tachykinin |
| 144 | 27 | 100.0 | 11 | 4 | AAH91449 | harr91449 Tachykinin |
| 145 | 27 | 100.0 | 11 | 4 | AAH91402 | harr91402 Tachykinin |
| 146 | 27 | 100.0 | 11 | 4 | AAH91436 | harr91436 Tachykinin |
| 147 | 27 | 100.0 | 11 | 4 | AAG9358 | hagg9358 ATT-short |
| 148 | 27 | 100.0 | 11 | 4 | AAG9354 | hagg9354 Substance |
| 149 | 27 | 100.0 | 11 | 4 | AAG9337 | hagg9337 Human aty |
| 150 | 27 | 100.0 | 11 | 4 | AAU07298 | hau07298 Substance |

ALIGNMENTS

RESULT:
 ID AAR33009
 AAR33009 standard; peptide; 5 AA.
 XX
 AC AAR33009;
 XX
 DT 25-MAR-2003 (revised)
 02-APR-1993 (first entry)
 XX
 DE Alpha-substituted short peptide.
 XX
 KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
 improved bioavailability.
 XX
 DS Synthetic.
 XX

| | | |
|----------|-----------------------------------|---|
| FT | Key | Location/Qualifiers |
| FT | Modified-site | 4 /note= "alpha-Me-Leu" |
| FT | Modified-site | 5 /note= "Met-NH2" |
| FT | | |
| PN | WO9219254-A1. | |
| XX | 12-NOV-1992. | |
| XX | 15-APR-1992; | 92WO-US003119. |
| PF | PR | 24-APR-1991; 91US-00690755. |
| XX | PR | 20-MAR-1992; 92US-00852086. |
| XX | XX | (WARN) WARNER LAMBERT CO. |
| PA | PI | Horwell DC, Hughes J, Richardson RS, Howson W; |
| XX | DR | WPI; 1992-398522/48. |
| XX | PS | New alpha-subst. polypeptide are e.g. selective receptor ligands - for |
| PT | CC | treating inflammation, pain, stroke, ulcers, hypertension, heart failure, |
| PT | CC | depression, cancer, asthma, psychosis, arthritis, etc. |
| PT | CC | The peptide is a specifically claimed example of a group of generically |
| PT | CC | claimed mono-, di-, tri-, tetra- and penta-peptides which include a |
| PT | CC | substituent on an alpha-C atom in the chain. Such substitution may modify |
| PT | CC | the bioavailability, stability or absorbability of the peptide and hence |
| PT | CC | may improve the activity of the peptide as a drug. Depending on the |
| PT | CC | nature of the parent peptide (hormone, endorphin, CCK, NK2 chemotactic |
| PT | CC | peptide, etc.), the modified peptides are variously useful for treating |
| PT | CC | obesity, anxiety, gastrointestinal ulcers, pain, stroke, inflammation, |
| PT | CC | addictive drug withdrawal symptoms, hypertension, heart failure, |
| PT | CC | cognition or memory disorders, spasticity, depression, diabetes, cancer, |
| PT | CC | asthma, bladder dysfunction, psychosis and arthritis; and as |
| PT | CC | contraceptives. (Updated on 25-MAR-2003 to correct PN field.) (Updated on |
| PT | CC | 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PR |
| PT | CC | field.) (Updated on 25-MAR-2003 to correct PI field.) |
| SQ | XX | Sequence 5 AA; |
| Query | Best Local Similarity | 100 %; Score 27; DB 2; Length 5; |
| Matches | Matches | 100 %; Pred No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 | FPGLM 5 |
| Db | 1 | FPGLM 5 |
| RESULT 2 | | |
| ID | AAR33008 | |
| AC | AAR33008 standard; Peptide; 5 AA. | |
| AC | AAR33008; | |
| DT | 25-MAR-2003 (revised) | |
| DT | 02-APR-1993 (first entry) | |
| XX | DE | Alpha-substituted short Peptide. |
| XX | KW | CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia; |
| XX | KW | improved bioavailability. |
| OS | OS | Synthetic. |
| FF | Key | Location/Qualifiers |
| FT | Modified-site | 2 /note= "alpha-Me-Phe" |
| FT | Modified-site | 5 |

GenCore version 5.1.6
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Om protein - protein search, using SW model

Run on: October 26, 2005, 08:01:20 ; Search time 102.222 Seconds

(without alignments)
20.038 Million cell updates/sec

Title: US-240-053-669-2

Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62 . Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB-seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 150 summaries

- Database : 1: uniprot_sprot: *
2: uniprot_trembl: *
- pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------------------|
| 1 | 21 | 100.0 | 11 1 | TNA4_PSEGU | P42989 pseudophryn pseudophryn |
| 2 | 21 | 100.0 | 11 1 | TNA4_PSEGU | P42990 pseudophryn pseudophryn |
| 3 | 21 | 100.0 | 11 1 | TNA4_CAVPO | P67932 cavia porce |
| 4 | 21 | 100.0 | 11 1 | TNA4_CHICK | P19850 gallus gallus |
| 5 | 21 | 100.0 | 11 1 | TNA4_HORSE | P67933 equus cabal |
| 6 | 21 | 100.0 | 11 1 | TNA4_ONCMI | P21499 oncorhynchus |
| 7 | 21 | 100.0 | 11 1 | TNA4_SCYCA | P1333 scyllorhinus |
| 8 | 21 | 100.0 | 19 1 | PAS2_HUMAN | P4606 homo sapien |
| 9 | 21 | 100.0 | 19 2 | Q9SBZ2 | Q98Be2 spinacia ol |
| 10 | 21 | 100.0 | 41 2 | Q7UFM5 | Q9fUm5 rhodopirell |
| 11 | 21 | 100.0 | 45 2 | Q6LD93 | Q6ld93 rattus sp. |
| 12 | 21 | 100.0 | 46 2 | Q87Rm6 | Q87Rm6 vibrio para |
| 13 | 21 | 100.0 | 53 2 | Q9TYI4 | Q9yi4 caenorhabdi |
| 14 | 21 | 100.0 | 55 2 | Q17544 | Q17544 caenorhabdi |
| 15 | 21 | 100.0 | 55 2 | Q04360 | Q04360 ceratitis c |
| 16 | 21 | 100.0 | 56 1 | YRZK_BACSU | Q32040 bacillus su |
| 17 | 21 | 100.0 | 58 2 | Q8Emw4 | Q8Emw4 oceanobacill |
| 18 | 21 | 100.0 | 63 2 | Q6RIAO | Q6ria0 nematostell |
| 19 | 21 | 100.0 | 63 2 | Q9GMU1 | Q9gm1 macaca fasc |
| 20 | 21 | 100.0 | 63 2 | Q6BQ3 | Q6Bq3 oryza sativ |
| 21 | 21 | 100.0 | 63 2 | Q82X04 | Q82x04 nitrosomona |
| 22 | 21 | 100.0 | 64 2 | Q86H30 | Q86h30 dictyosteli |
| 23 | 21 | 100.0 | 67 2 | Q8TLY1 | Q8tly1 methanosarc |
| 24 | 21 | 100.0 | 67 2 | Q8GRG4 | Q8grg4 lycopersico |
| 25 | 21 | 100.0 | 68 2 | Q05825 | Q05825 staphylococ |
| 26 | 21 | 100.0 | 68 2 | Q50886 | Q50886 myxococcus |
| 27 | 21 | 100.0 | 69 1 | Y010_TROWB | P67379 tropheryma |
| 28 | 21 | 100.0 | 69 1 | Y010_TROWT | P67378 tropheryma |
| 29 | 21 | 100.0 | 69 1 | YATI_RHOBL | P05443 rhodopseudoo |
| 30 | 21 | 100.0 | 72 2 | Q9Y474 | Q9y474 homo sapien |
| 31 | 21 | 100.0 | 72 2 | Q9GP92 | Q9gp92 caenorhabdai |
| 32 | 21 | 100.0 | 72 2 | Q8CSF7 | Q8csf7 staphylococ |
| 33 | 21 | 100.0 | 74 2 | Q8IWZ7 | Q8iwz7 homo sapien |
| 34 | 21 | 100.0 | 76 2 | Q86TU6 | Q86tu6 homo sapien |
| 35 | 21 | 100.0 | 78 2 | Q8VW82 | Q8vw82 colwellia m |
| 36 | 21 | 100.0 | 78 2 | Q8UKQ3 | Q8ukq3 agrobacteri |
| 37 | 21 | 100.0 | 79 2 | Q8RH49 | Q8rh49 brugia mala |
| 38 | 21 | 100.0 | 79 2 | Q8K214 | Q8k214 uncultured |
| 39 | 21 | 100.0 | 80 2 | Q47577 | Q47577 onchocerca |
| 40 | 21 | 100.0 | 80 2 | Q9BN11 | Q9bn11 rhizobium l |
| 41 | 21 | 100.0 | 81 2 | Q8XH79 | Q8xh79 clostridium |
| 42 | 21 | 100.0 | 81 2 | Q7MD50 | Q7md50 streptococc |
| 43 | 21 | 100.0 | 81 2 | Q8D627 | Q8d627 vibrio vuln |
| 44 | 21 | 100.0 | 82 2 | Q6ECK5 | Q6eck5 oryctolagus |
| 45 | 21 | 100.0 | 83 2 | Q6TRW3 | Q6trw3 sulfolobus |
| 46 | 21 | 100.0 | 84 2 | Q6YMP5 | Q6ymp5 arytina de |
| 47 | 21 | 100.0 | 84 2 | Q6YNP7 | Q6ynp7 arytina de |
| 48 | 21 | 100.0 | 88 2 | Q7U6H0 | Q7u6h0 rhodopirell |
| 49 | 21 | 100.0 | 89 2 | Q49761 | Q49761 mycobacteri |
| 50 | 21 | 100.0 | 90 1 | Y040_CORGI | Q68385 carnation m |
| 51 | 21 | 100.0 | 90 1 | YFIM_ECOLI | Q26173 methanobact |
| 52 | 21 | 100.0 | 90 1 | Q8H8X0 | Q75556 methanobact |
| 53 | 21 | 100.0 | 90 2 | Q94J6M | Q9jmg6 oryza sativ |
| 54 | 21 | 100.0 | 90 2 | Q7UBW7 | Q86u7 vibriophage |
| 55 | 21 | 100.0 | 90 2 | Q8XFR4 | Q89f4 escherichia |
| 56 | 21 | 100.0 | 90 1 | Q589H4 | Q658h4 oryza sativ |
| 57 | 21 | 100.0 | 90 1 | Q920K2 | Q92916 escherichia |
| 58 | 21 | 100.0 | 90 1 | Q9R0D7 | Q75556 methanobact |
| 59 | 21 | 100.0 | 90 2 | Q63W33 | Q6eck6 oryctolagus |
| 60 | 21 | 100.0 | 90 2 | Q9XG57 | Q63W33 burkholderi |
| 61 | 21 | 100.0 | 97 2 | Q6974 | Q9yg57 aeropyrum p |
| 62 | 21 | 100.0 | 97 2 | Q92K16 | Q68974 synedhococc |
| 63 | 21 | 100.0 | 95 1 | MGBB_HUMAN | Q92916 escherichia |
| 64 | 21 | 100.0 | 96 1 | Y87A_HAEIN | Q75556 methanobact |
| 65 | 21 | 100.0 | 96 1 | Q9N0E2 | Q6eck6 oryctolagus |
| 66 | 21 | 100.0 | 96 2 | Q86TU8 | Q6eck6 oryctolagus |
| 67 | 21 | 100.0 | 96 2 | Q9XG57 | Q63W33 burkholderi |
| 68 | 21 | 100.0 | 97 2 | Q6SGM8 | Q68974 synedhococc |
| 69 | 21 | 100.0 | 97 2 | Q92K16 | Q92916 rhizobium m |
| 70 | 21 | 100.0 | 97 2 | Q92K16 | Q92916 rhizobium m |
| 71 | 21 | 100.0 | 100 2 | Q9VCL2 | Q7vcl12 prochlorococ |
| 72 | 21 | 100.0 | 104 2 | Q9TC76 | Q9yc76 aeropyrum p |
| 73 | 21 | 100.0 | 104 2 | Q9PMX7 | Q9pmx7 campylobact |
| 74 | 21 | 100.0 | 104 2 | Q9ECK8 | Q6eck8 homo sapien |
| 75 | 21 | 100.0 | 104 2 | Q92K16 | Q7x2c5 rhodococcus |
| 76 | 21 | 100.0 | 104 2 | Q92K16 | Q6nbv3 rhodopseu |
| 77 | 21 | 100.0 | 105 2 | Q9E5Z7 | Q8e5z7 streptococc |
| 78 | 21 | 100.0 | 105 2 | Q9FWT0 | Q8fwt0 brucella su |
| 79 | 21 | 100.0 | 107 2 | Q96G049 | Q16164 homo sapien |
| 80 | 21 | 100.0 | 107 2 | Q7X2C5 | Q9949 phage phim |
| 81 | 21 | 100.0 | 107 2 | Q6NBV3 | Q7x2c5 rhodococcus |
| 82 | 21 | 100.0 | 107 2 | Q8E5Z7 | Q8e5z7 streptococc |
| 83 | 21 | 100.0 | 108 2 | Q9FWT0 | Q8fwt0 brucella su |
| 84 | 21 | 100.0 | 109 2 | Q96I64 | Q16164 homo sapien |
| 85 | 21 | 100.0 | 109 2 | Q96G049 | Q9949 phage phim |
| 86 | 21 | 100.0 | 109 2 | Q887P1 | Q8h7p1 oryza sativ |
| 87 | 21 | 100.0 | 109 2 | Q6SK09 | Q6sk09 bacillus li |
| 88 | 21 | 100.0 | 109 2 | Q81X85 | Q81x85 bacillus an |
| 89 | 21 | 100.0 | 110 1 | COK4_BACSU | P24013 bacillus su |
| 90 | 21 | 100.0 | 111 1 | Q6N195 | Q6n195 methanococc |
| 91 | 21 | 100.0 | 112 2 | Q9X54 | Q9xe54 arabidopsis |
| 92 | 21 | 100.0 | 113 2 | Q86TU9 | Q86uu9 homo sapien |
| 93 | 21 | 100.0 | 113 2 | Q7NHZ1 | Q7nhz1 gloeobacter |
| 94 | 21 | 100.0 | 114 1 | Y65_METRA | Q58891 methanococc |
| 95 | 21 | 100.0 | 114 2 | Q7Y947 | Q97947 tulpia glis |
| 96 | 21 | 100.0 | 114 2 | Q83K17 | Q83k17 shigella fl |
| 97 | 21 | 100.0 | 114 2 | Q8F03 | Q8ff03 escherichia |
| 98 | 21 | 100.0 | 115 1 | TK01_RABIT | Q8ff03 escherichia |
| 99 | 21 | 100.0 | 115 2 | Q6W4R0 | Q6w4r0 vibrio angu |
| 100 | 21 | 100.0 | 115 2 | Q920K1 | Q920k1 cavia porce |
| 101 | 21 | 100.0 | 116 2 | Q67UV6 | Q6yuv6 oryza sativ |
| 102 | 21 | 100.0 | 116 2 | Q9HG9 | Q9hxg9 pseudomonas |
| 103 | 21 | 100.0 | 116 2 | Q9X1V2 | Q9x1v2 thermotoga |
| 104 | 21 | 100.0 | 117 1 | NU3M_BRALIA | Q47429 branchiost |

| RESULT 1 | | | | | |
|--|-----------|------|--------|-----|----|
| KN4_PSGU | STANDARD; | PRT; | 11 AA. | | |
| PA2989; 01-NOV-1995 (Rel. 32, Created) 05-JUL-2004 (Rel. 44, Last annotation update) | | | | | |
| Substance P-like peptide I | | | | | |
| Pseudophryne guentheri (Guenther's broadleaf tree frog) | | | | | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batracia; Anura; Neobatrachia; Hyloidea; Myobatrachidae; Myobatrachinae; Pseudophryne. | | | | | |
| [NCBI_TAXID=30349;] | | | | | |
| SEQUENCE: | | | | | |
| TISSUE:Skin secretion; | | | | | |
| MEDLINE#90287814; Published=2356157; DOI=10.1016/0196-9781(90)90086-K; | | | | | |
| Simmaco M., Severini C. de Biasi D., Barra D., Bossa F., | | | | | |
| Roberts J.D., Melchiorri P., Espamer V., | | | | | |
| "Six novel tachykinin- and bombesin-related peptides from the Australian frog Pseudophryne guentheri."; | | | | | |
| Proc Natl Acad Sci USA 87:1299-1304 (1990) | | | | | |
| [1] | | | | | |
| ALIGNMENTS | | | | | |
| Q85CK1 branchiostoto | Q85CK1 | 117 | 2 | 117 | 21 |
| Q85CK8 brachiooste | Q85CK8 | 106 | 2 | 100 | 21 |
| Q85K8 branchiostoto | Q85K8 | 107 | 2 | 100 | 21 |
| Q76FAB pasteurella | Q76FAB | 108 | 2 | 100 | 21 |
| Q76FAB pasteurella | Q76FAB | 109 | 2 | 100 | 21 |
| Q7WRP9 anaerbaena ci | Q7WRP9 | 110 | 2 | 100 | 21 |
| Q7WRP9 anaerbaena ci | Q7WRP9 | 111 | 2 | 100 | 21 |
| Q94QPS inversdens | Q94QPS | 112 | 2 | 100 | 21 |
| Q6XYC2 homo sapien | Q6XYC2 | 113 | 2 | 100 | 21 |
| Q6XYC2 homo sapien | Q6XYC2 | 114 | 2 | 100 | 21 |
| Q8FTN5 escherichia | Q8FTN5 | 115 | 2 | 100 | 21 |
| Q8FTN5 escherichia | Q8FTN5 | 116 | 2 | 100 | 21 |
| Q8VH12 ractus norv | Q8VH12 | 117 | 2 | 100 | 21 |
| Q8VH12 ractus norv | Q8VH12 | 118 | 2 | 100 | 21 |
| Q8B8J9 calyptogena | Q8B8J9 | 119 | 2 | 100 | 21 |
| Q87114 vibrio para | Q87114 | 120 | 2 | 100 | 21 |
| Q87VPH0 pseudomonas | Q87VPH0 | 121 | 2 | 100 | 21 |
| Q20366 homo sapien | Q20366 | 122 | 2 | 100 | 21 |
| Q9K8M3 virio chol | Q9K8M3 | 123 | 2 | 100 | 21 |
| Q977948 tuparia glis | Q977948 | 124 | 2 | 100 | 21 |
| P01289 bos taurus | P01289 | 125 | 2 | 100 | 21 |
| Q65501 mesocricetus | Q65501 | 126 | 2 | 100 | 21 |
| P41539 mus musculus | P41539 | 127 | 2 | 100 | 21 |
| P06767 ractus norv | P06767 | 128 | 2 | 100 | 21 |
| Q9ZOK0 cavia porce | Q9ZOK0 | 129 | 2 | 100 | 21 |
| P59832 Klebsiella | P59832 | 130 | 2 | 100 | 21 |
| Q8Z1D6 Yersinia ps | Q8Z1D6 | 131 | 2 | 100 | 21 |
| Q8Z1D6 Yersinia ps | Q8Z1D6 | 132 | 1 | 100 | 21 |
| Q1OTR CHICK | Q1OTR | 133 | 1 | 100 | 21 |
| Q8XPR8 salmonella | Q8XPR8 | 134 | 1 | 100 | 21 |
| Q7CR2 salmonella | Q7CR2 | 135 | 2 | 100 | 21 |
| Q26397 methanobact | Q26397 | 136 | 2 | 100 | 21 |
| Q9N3Y5 caenorhabdi | Q9N3Y5 | 137 | 2 | 100 | 21 |
| Q7n098 photorhabdu | Q7n098 | 138 | 2 | 100 | 21 |
| Q18P6 gallus galli | Q18P6 | 139 | 2 | 100 | 21 |
| Q8FXR8 salmonella | Q8FXR8 | 140 | 2 | 100 | 21 |
| Q26397 shigella fl | Q26397 | 141 | 2 | 100 | 21 |
| Q68699 yersinia pe | Q68699 | 142 | 2 | 100 | 21 |
| Q87T99 vibrio para | Q87T99 | 143 | 2 | 100 | 21 |
| Q8ETC0 oceanobacil | Q8ETC0 | 144 | 2 | 100 | 21 |
| Q8FRD4 escherichia | Q8FRD4 | 145 | 2 | 100 | 21 |
| Q8P4585 escherichia | Q8P4585 | 146 | 2 | 100 | 21 |
| P64587 shigella fl | P64587 | 147 | 2 | 100 | 21 |
| Q8BKG1 chlorobium | Q8BKG1 | 148 | 2 | 100 | 21 |
| Q68699 yersinia pe | Q68699 | 149 | 2 | 100 | 21 |
| Q86W44 mycoplasma | Q86W44 | 150 | 2 | 100 | 21 |
| Q6bbjs calyptogena | Q6bbjs | | | | |

ALIGNMENTS

| ALIGNMENTS | | | | | |
|---|-----------|------|--------|---|--|
| RESULT 1 | | | | | |
| CN4_PSGU | STANDARD; | PRT; | 11 AA. | | |
| TGN4_PSGU | | | | P42989; | |
| | | | | 01-NOV-1995 (Rel. 32, Created) | |
| | | | | 01-NOV-1995 (Rel. 32, Last sequence update) | |
| | | | | 03-JUL-2004 (Rel. 44, Last annotation update) | |
| | | | | Substance P-like Peptide I (PG-SPI). | |
| | | | | Pseudophryne guentheri (Guenther's toadlet). | |
| | | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | | | | Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; | |
| | | | | Myobatrachidae; Myobatrachidae; | |
| | | | | Neobi1_TaxID=30349; | |
| | [1] | | | | |
| SEQUENCE | | | | | |
| TISSUESkin Secretion; | | | | | |
| MIDDLENAME=90287814; Published=2356157; DOI=10.1016/0195-9781(90)90086-K; | | | | | |
| Simmaco M., Severeini C., de Biase D., Bassa D., Bossa F., | | | | | |
| Robert J.D., Melchiorri P., Esparmer V., | | | | | |
| "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.", | | | | | |
| peptides 11:299-304 (1990) | | | | | |

RT
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guntheri*.";
 RL
 Peptides 11:299-304 (1990).
 CC
 -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasoconstrictors and secretagogues, and contract (directly or indirectly) many smooth muscle.
 CC
 -!- SUBCELLULAR LOCATION: Secreted.
 CC
 -!- TISSUE SPECIFICITY: Skin.
 CC
 -!- SIMILARITY: Belongs to the tachykinin family.
 DR
 PIR; F60409; F60409.
 DR
 IPIDPro; IPD00240; Tachy-Neurokinin.
 DR
 Pfam; PF02202; Tachykinin_1.
 DR
 PROSITE; PS00267; TACHYKININ_1.
 KW
 Amidated neuropeptide; Direct protein sequencing;
 KW
 Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
 FT
 Pyrrolidone carboxylic acid.
 MOD RES
 1
 11
 11
 Methionine amide.
 FT
 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
 SQ
 SEQUENCE
 100 %; Score 21; DB 1; Length 11;
 Best Local Similarity 100 %; Pred. No. 2e-02; Mismatches 0; Indels 0; Gaps 0
 Query Match
 Best Local Similarity 100 %; Pred. No. 2e-02; Mismatches 0; Indels 0; Gaps 0
 Matches 4; Conservative 0; Misaligned 0
 QY 1 FGIM 4

| OM protein - protein search, using SW model | | | | | | |
|--|-------|--------------------|--------------|--------------------|--|-----|
| Run on: October 26, 2005, 08:04:16 ; Search time 10.6667 Seconds | | | | | | 331 |
| (without alignment) | | | | | | 332 |
| 36.081 Million cell updates/sec | | | | | | 333 |
| Title: US-10-0537669-2 | | | | | | 334 |
| Sequence: 1-PFGM 4 | | | | | | 335 |
| Scoring table: BL0SUM62 | | | | | | 336 |
| Gapop 10.0 , Gapext 0.5 | | | | | | 337 |
| Searched: 283416 seqs, 96216763 residues | | | | | | 338 |
| Total number of hits satisfying chosen parameters: 283416 | | | | | | 339 |
| Minimum DB seq length: 0 | | | | | | 340 |
| Maximum DB seq length: 2000000000 | | | | | | 341 |
| Post-processing: Minimum Match 0% | | | | | | 342 |
| Database : PIR 79;* | | | | | | 343 |
| 1: p1x1;* | | | | | | 344 |
| 2: p1x2;* | | | | | | 345 |
| 3: p1x3;* | | | | | | 346 |
| 4: p1x4;* | | | | | | 347 |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | | | |
| SUMMARIES | | | | | | |
| Result No. | Score | Query Match Length | DB ID | Description | | |
| 1 | 21 | 100.0 | 11 1 A60524 | substance P - guin | | |
| 2 | 21 | 100.0 | 11 1 SPHO | substance P - hors | | |
| 3 | 21 | 100.0 | 11 2 JN0023 | substance P - chic | | |
| 4 | 21 | 100.0 | 11 2 S33300 | probable substance | | |
| 5 | 21 | 100.0 | 11 2 E60409 | substance P-like p | | |
| 6 | 21 | 100.0 | 11 2 F60409 | substance P - rain | | |
| 7 | 21 | 100.0 | 11 2 PS0332 | phospholipase A2 (| | |
| 8 | 21 | 100.0 | 19 2 A69983 | hypothetical prote | | |
| 9 | 21 | 100.0 | 63 2 JC2412 | tachykinin gamma c | | |
| 10 | 21 | 100.0 | 69 2 S04666 | hypothetical prote | | |
| 11 | 21 | 100.0 | 72 2 JC5435 | preprotachykinin-A | | |
| 12 | 21 | 100.0 | 72 2 T25860 | tachykinin A gamma | | |
| 13 | 21 | 100.0 | 72 2 AE3105 | hypothetical prote | | |
| 14 | 21 | 100.0 | 78 2 T11059 | hypothetical prote | | |
| 15 | 21 | 100.0 | 80 2 H69191 | NADH dehydrogenas | | |
| 16 | 21 | 100.0 | 85 2 H69191 | hypothetical prote | | |
| 17 | 21 | 100.0 | 89 2 S72598 | sulfate permease T | | |
| 18 | 21 | 100.0 | 90 2 C85905 | hypothetical prote | | |
| 19 | 21 | 100.0 | 90 2 E91060 | hypothetical prote | | |
| 20 | 21 | 100.0 | 90 2 A65037 | hypothetical prote | | |
| 21 | 21 | 100.0 | 97 2 S12958 | tachykinin delta p | | |
| 22 | 21 | 100.0 | 102 2 Q72756 | hypothetical prote | | |
| 23 | 21 | 100.0 | 105 2 F72634 | hypothetical prote | | |
| 24 | 21 | 100.0 | 106 2 G81276 | hypothetical prote | | |
| 25 | 21 | 100.0 | 109 2 I52333 | Gl phase-specific | | |
| 26 | 21 | 100.0 | 110 2 G69609 | cytochrome-c oxiда | | |
| 27 | 21 | 100.0 | 112 2 SPRTA | substance P alpha | | |
| 28 | 21 | 100.0 | 112 2 TS1238 | scarerow-like pro | | |
| 29 | 21 | 100.0 | 112 2 A95362 | | | |

RESULT 1

Substance P - guinea pig
 Species: *Cavia porcellus* (guinea pig)
 Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 Accession: A60654
 Molecule type: protein
 Residues: 1-11 <MUR>

A;Title: Primary amino acid sequence of guinea-pig substance P.
 A;Title: Reference number: A60654; MUID:90044685; PMID:2478925
 A;Accession: A60654
 C;Species: amiodated carboxyl end; tachykinin
 C;KeyWord: amidated carboxyl end (Met) #status experimental
 F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 8 FGIM 11

RESULT 2

Substance P - horse
 Species: *Equus caballus* (domestic horse)
 Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
 Accession: A01558
 Author, R.O.; Tzecak, A.; Lergier, W.
 Helv. Chim. Acta 56, 860-866, 1973
 Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
 Reference number: A01558
 Accession: A01558
 Molecule type: protein
 Residues: 1-11 <STU>
 Cross-references: UNIPROT:PO1290
 Superfamily: substance P precursor
 Keywords: amidated arboxyl end; hormone
 Modified site: amidated carboxyl end (Met) #status experimental

Query Match 100.0%; Score 21; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 8 FGIM 11

RESULT 3

Substance P - chicken
 Species: *Gallus gallus* (chicken)
 Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 Accession: JN0023
 Author, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
 Regul. Pept. 20, 177-180, 1988
 Title: Arg3 substance P and neurokinin A from chicken small intestine.
 Reference number: JN0023; MUID:88204263; PMID:2452461
 Accession: JN0023
 Molecule type: protein
 Residues: 1-11 <CON>
 Cross-references: UNIPROT:PI19850
 Superfamily: substance P precursor
 Keywords: amidated carboxyl end; tachykinin
 Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 8 FGIM 11

RESULT 4

Substance P - smaller spotted catshark
 Species: *Scyliorhinus canicula* (smaller spotted catshark, smaller spotted dogfish)
 Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 Accession: S33300
 Author, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.
 Biochem. 214, 469-474, 1993
 Title: Primary structures and biological activities of substance-P-related peptides from
 Reference number: S33300; MUID:93292508; PMID:7685693
 Accession: S33300
 Molecule type: protein

RESULT 1

Substance P - guinea pig
 Species: *Cavia porcellus* (guinea pig)
 Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 Accession: A60654
 Molecule type: protein
 Residues: 1-11 <MUR>

A;Title: Primary amino acid sequence of guinea-pig substance P.
 A;Title: Reference number: A60654; MUID:90044685; PMID:2478925
 A;Accession: A60654
 C;Species: amiodated carboxyl end; tachykinin
 C;KeyWord: amidated carboxyl end (Met) #status experimental
 F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 21; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 26, 2005, 08:05:47 ; Search time 99.5556 Seconds
(without alignments)
16.775 Million cell updates/sec

Title: ~~US-10-053-669-2_1.rapb~~
Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Database ~~Published Applications~~ ~~Non-GenBank~~
Listing first 150 summaries

| Result NO. | Score | Query | Match Length | DB ID | Description |
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| 2 | 21 | 100.0 | 4 | 14 US-10-230-13-3 | Sequence 3, Appli |
| 3 | 21 | 100.0 | 4 | 14 US-10-033-669-2 | Sequence 2, Appli |
| 4 | 21 | 100.0 | 4 | 16 US-10-695-536-3 | Sequence 3, Appli |
| 5 | 21 | 100.0 | 4 | 16 US-10-805-881-2 | Sequence 2, Appli |
| 6 | 21 | 100.0 | 4 | 17 US-10-497-628-2 | Sequence 2, Appli |
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| 8 | 21 | 100.0 | 4 | 20 US-11-056-697-623 | Sequence 623, Appli |
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| 12 | 21 | 100.0 | 5 | 16 US-10-688-741-3 | Sequence 3, Appli |
| 13 | 21 | 100.0 | 5 | 16 US-10-346-737A-30 | Sequence 1, Appli |
| 14 | 21 | 100.0 | 5 | 16 US-10-805-881-1 | Sequence 3, Appli |
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| 26 | 21 | 100.0 | 6 | 20 US-11-066-697-597 | Sequence 597, App |
| 27 | 21 | 100.0 | 6 | 20 US-11-066-697-601 | Sequence 601, App |
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| 66 | 21 | 100.0 | 11 | 14 US-10-053-669-3 | Sequence 3, Appli |
| 67 | 21 | 100.0 | 11 | 14 US-10-211-994-3 | Sequence 3, Appli |
| 68 | 21 | 100.0 | 11 | 14 US-10-114-023B-24 | Sequence 24, Appli |
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Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 21 | 100.0 | 4 | 14 US-10-033-669-2 | Sequence 2, Appli |
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| 8 | 21 | 100.0 | 4 | 20 US-11-056-697-623 | Sequence 623, Appli |
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RESULT 2
US-10-230-133-3
; Sequence 3, Application US/10230133
; Publication No. US20030040625A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and methods for treatment of abnormal physiological states
; FILE REFERENCE: 2892-106
; CURRENT APPLICATION NUMBER: US/10/230,133
; CURRENT FILING DATE: 2003-08-29
; PRIORITY APPLICATION NUMBER: 09/635,266
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: AMIDATION
US-10-230-133-3

Query Match 100.0%; Score 21; DB 14; Length 4;
Best Local Similarity 100.0%; Pred No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 FGIM 4
Db 1 FGIM 4

RESULT 3
US-10-053-669-2
; Sequence 2, Application US/10053669
; Publication No. US20030077658A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Ibert
; TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
; FILE REFERENCE: NI427-005

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 Db 1 FGIM 4

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 COMPUTER TYPE: Diskette, 3.50 inch, 1.44 MG storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/441,591
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/3/03, 362
 FILING DATE: 9-SEPTEMBER-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/117, 991
 FILING DATE: 10-JUNE-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/931, 473
 FILING DATE: 17-AUGUST-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/954, 624
 FILING DATE: 21-OCTOBER-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33, 215
 REFERENCE DOCKET NUMBER: NEX21/C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEX/FAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-441-591-63

RESULT 1
 US-08-441-591-63
 Sequence 63, Application US/08441591
 ; Sequence 63, Application US/08441591
 ; GENERAL INFORMATION:
 ; APPLICANT: NIEUMANDT, D., GOLD, L. AND WECKER, M.
 ; TITLE OF INVENTION: HIGH-AFFINITY
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
 ; TITLE OF INVENTION: TO THE TACHYKININ
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80111

RESULT 2
 US-08-303-362A-63
 ; Sequence 63, Application US/08303362A
 ; Patent No. 5,948214
 ; GENERAL INFORMATION:
 ; APPLICANT: NIEUMANDT, D., GOLD, L. AND WECKER, M.
 ; TITLE OF INVENTION: HIGH-AFFINITY
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
 ; TITLE OF INVENTION: TO THE TACHYKININ
 ; TITLE OF INVENTION: SUBSTANCE P
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80111
 ; COMPUTER READABLE FORM:
 ; COMPUTER TYPE: Disquette, 3.50 inch, 1.44 MG storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS-DOS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using sw model
Run on: October 26, 2005, 08:00:50 ; Search time 57.7778 seconds
(without alignments)
26.776 Million cell updates/sec

Title: Perfect score: 21

Sequence: 1 FGLM 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

POST-processing: Maximum Match 0%
Listing first 150 summaries

Databaser: 1: GeneSeq, 2: Geddec04, *:

1: geneseqD1980B: *
2: geneseqD1990B: *
3: geneseqD2000B: *
4: geneseqD2001B: *
5: geneseqD2002B: *
6: geneseqD2003B: *
7: geneseqD2003B: *
8: geneseqD2004B: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|----------------------|
| 1 | 21 | 100.0 | 4 2 | AAW41683 Peptide u |
| 2 | 21 | 100.0 | 4 2 | AAV31075 Non-cross |
| 3 | 21 | 100.0 | 4 3 | AAB23026 Human/rat |
| 4 | 21 | 100.0 | 4 3 | AYY7577 P antagonist |
| 5 | 21 | 100.0 | 4 4 | AAB91447 Tachykinin |
| 6 | 21 | 100.0 | 4 4 | ABB10091 Substance |
| 7 | 21 | 100.0 | 4 5 | AAU77846 Tachykinin |
| 8 | 21 | 100.0 | 4 7 | ADP84198 High acti |
| 9 | 21 | 100.0 | 4 7 | ADR3772 Human mag |
| 10 | 21 | 100.0 | 5 2 | AAB33009 Alpha-sub |
| 11 | 21 | 100.0 | 5 2 | ARR23008 Alpha-sub |
| 12 | 21 | 100.0 | 5 2 | AAR33007 Alpha-sub |
| 13 | 21 | 100.0 | 5 2 | AAB33010 Alpha-sub |
| 14 | 21 | 100.0 | 5 2 | ARR45459 Cholecyt |
| 15 | 21 | 100.0 | 5 2 | ARR45511 Cholecyt |
| 16 | 21 | 100.0 | 5 2 | ARR4550 Cholecyt |
| 17 | 21 | 100.0 | 5 2 | ARR4548 Cholecyt |
| 18 | 21 | 100.0 | 5 2 | ARR41687 Teprilapt |
| 19 | 21 | 100.0 | 5 2 | AAW99643 Substance |
| 20 | 21 | 100.0 | 5 2 | AYP50325 Neutrophi |
| 21 | 21 | 100.0 | 5 2 | Raw9260 Human tac |
| 22 | 21 | 100.0 | 5 2 | Raw92702 Human tac |
| 23 | 21 | 100.0 | 5 3 | ABZ23025 Human/rat |
| 24 | 21 | 100.0 | 5 3 | AYY7576 P antagonist |
| 25 | 21 | 100.0 | 5 4 | AAB91428 Tachykinin |

| | | | | |
|----|----|-------|-----|-----------------------|
| 26 | 21 | 100.0 | 5 4 | AAB91389 Tachykinin |
| 27 | 21 | 100.0 | 5 5 | Abb11389 Tachykinin |
| 28 | 21 | 100.0 | 5 5 | Abb1090 Substance |
| 29 | 21 | 100.0 | 5 5 | Abb1089 Substance |
| 30 | 21 | 100.0 | 5 5 | Abb1088 Substance |
| 31 | 21 | 100.0 | 5 5 | AAU77845 Tachykinin |
| 32 | 21 | 100.0 | 5 5 | Ade94205 High acti |
| 33 | 21 | 100.0 | 5 5 | ADB94203 High acti |
| 34 | 21 | 100.0 | 5 5 | ADB94204 High acti |
| 35 | 21 | 100.0 | 5 5 | ADB92530 Substance |
| 36 | 21 | 100.0 | 5 5 | ADN95078 Mammalian |
| 37 | 21 | 100.0 | 5 5 | ADR03603 E. coli m |
| 38 | 21 | 100.0 | 5 5 | Ade43771 Human mag |
| 39 | 21 | 100.0 | 5 5 | AAP40519 High acti |
| 40 | 21 | 100.0 | 5 5 | AAP50694 Sequence |
| 41 | 21 | 100.0 | 5 6 | AAP50322 Substance |
| 42 | 21 | 100.0 | 5 6 | AAP61486 Peptide h |
| 43 | 21 | 100.0 | 5 6 | AAR07893 Cyclic pept |
| 44 | 21 | 100.0 | 5 6 | Aar07899 Cyclic pept |
| 45 | 21 | 100.0 | 5 6 | Aar21959 Substance |
| 46 | 21 | 100.0 | 5 6 | Aar27690 Cyclic ta |
| 47 | 21 | 100.0 | 5 6 | Aar27694 Cyclic ta |
| 48 | 21 | 100.0 | 5 6 | Aar27691 Cyclic ta |
| 49 | 21 | 100.0 | 5 6 | AAM99692 Substance |
| 50 | 21 | 100.0 | 5 6 | AAM99686 Substance |
| 51 | 21 | 100.0 | 5 6 | Aaw92706 Human tac |
| 52 | 21 | 100.0 | 5 6 | Aaw92655 Human tac |
| 53 | 21 | 100.0 | 5 6 | Aab03356 Neurokin |
| 54 | 21 | 100.0 | 5 6 | AAY67575 P antagonist |
| 55 | 21 | 100.0 | 5 6 | AYV97917 Neurokin |
| 56 | 21 | 100.0 | 5 6 | AYV97947 Neurokin |
| 57 | 21 | 100.0 | 5 6 | AYV97932 Neurokin |
| 58 | 21 | 100.0 | 5 6 | AAB82453 Fluorinat |
| 59 | 21 | 100.0 | 5 6 | AAB82436 Fluorinat |
| 60 | 21 | 100.0 | 5 6 | AAB91421 Tachykinin |
| 61 | 21 | 100.0 | 5 6 | AAB91425 Tachykinin |
| 62 | 21 | 100.0 | 5 6 | AAB91390 Tachykinin |
| 63 | 21 | 100.0 | 5 6 | AAB91419 Tachykinin |
| 64 | 21 | 100.0 | 5 6 | AAG99351 Atypical |
| 65 | 21 | 100.0 | 5 6 | Aau07303 Human NK- |
| 66 | 21 | 100.0 | 5 6 | Aab88521 Human NK- |
| 67 | 21 | 100.0 | 5 6 | Ade94202 High acti |
| 68 | 21 | 100.0 | 5 6 | Adg9522 Substance |
| 69 | 21 | 100.0 | 5 6 | Abb10088 Substance |
| 70 | 21 | 100.0 | 5 6 | Abb21956 Substance |
| 71 | 21 | 100.0 | 5 6 | Ade94202 High acti |
| 72 | 21 | 100.0 | 5 7 | ADE94202 High acti |
| 73 | 21 | 100.0 | 5 7 | AAR21957 Substance |
| 74 | 21 | 100.0 | 5 7 | AAY50324 Neurophi |
| 75 | 21 | 100.0 | 5 7 | Aaw92662 Human tac |
| 76 | 21 | 100.0 | 5 7 | Aaw92705 Human tac |
| 77 | 21 | 100.0 | 5 7 | AAY67573 P antagonist |
| 78 | 21 | 100.0 | 5 7 | Aay67574 P antagonist |
| 79 | 21 | 100.0 | 5 7 | Aab80323 Human pro |
| 80 | 21 | 100.0 | 5 7 | Aab80324 Human pro |
| 81 | 21 | 100.0 | 5 7 | Aab91431 Tachykinin |
| 82 | 21 | 100.0 | 5 7 | Aab91420 Tachykinin |
| 83 | 21 | 100.0 | 5 7 | Aab91420 Tachykinin |
| 84 | 21 | 100.0 | 5 7 | AAB99350 Atypical |
| 85 | 21 | 100.0 | 5 7 | Aab98845 Chimeric |
| 86 | 21 | 100.0 | 5 7 | Abb09500 Substance |
| 87 | 21 | 100.0 | 5 7 | ADE94201 High acti |
| 88 | 21 | 100.0 | 5 7 | ADF92522 Substance |
| 89 | 21 | 100.0 | 5 8 | Adn95077 Mammalian |
| 90 | 21 | 100.0 | 5 8 | Aap20303 Gastroint |
| 91 | 21 | 100.0 | 5 8 | Aar84444 Neurokin |
| 92 | 21 | 100.0 | 5 8 | Aaw92664 Human tac |
| 93 | 21 | 100.0 | 5 8 | Aaw92710 Human tac |
| 94 | 21 | 100.0 | 5 8 | Aay67573 Atypical |
| 95 | 21 | 100.0 | 5 8 | Aab91407 Tachykinin |
| 96 | 21 | 100.0 | 5 8 | Aab91416 Tachykinin |
| 97 | 21 | 100.0 | 5 8 | Aab91424 Tachykinin |
| 98 | 21 | 100.0 | 5 8 | Aag99349 Atypical |
| 99 | 21 | 100.0 | 5 8 | Abb09498 Substance |

| | | | | | | | |
|-----|----|-------|--------------------------------|---|-----------|-------------------------------------|---|
| 99 | 21 | 100.0 | 8 | 7 | ADD94200 | Ade94200 High acti | FT Modified-site 4 /note= "C-terminal amide" |
| 100 | 21 | 100.0 | 9 | 1 | AAPE0334 | AAp50634 Substance | FT |
| 101 | 21 | 100.0 | 9 | 2 | AAW2714 | AAw92714 Human tac | XX |
| 102 | 21 | 100.0 | 9 | 4 | AA880325 | Ab880325 Human pro | PN |
| 103 | 21 | 100.0 | 9 | 4 | AB91446 | Ab91446 Tachykinin | XX |
| 104 | 21 | 100.0 | 9 | 4 | AB91369 | Ab91369 Tachykinin | PD |
| 105 | 21 | 100.0 | 9 | 4 | AAC99348 | Aag99348 Atypical | XX |
| 106 | 21 | 100.0 | 9 | 7 | AAE28833 | Aae3833 Membrane | PF |
| 107 | 21 | 100.0 | 9 | 7 | ADP2528 | Adf9228 Substance | XX |
| 108 | 21 | 100.0 | 9 | 8 | ADD04477 | Adc04477 Substance | PR |
| 109 | 21 | 100.0 | 9 | 8 | ADN95076 | Adn95076 Mammalian | XX |
| 110 | 21 | 100.0 | 9 | 8 | AD515335 | Aqb15335 Substance | PA |
| 111 | 21 | 100.0 | 10 | 1 | AAW50633 | Aap50633 Substance | XX |
| 112 | 21 | 100.0 | 10 | 2 | AAK21933 | Aar21933 Substance | PI |
| 113 | 21 | 100.0 | 10 | 2 | AAK5181 | Aar65181 S. cerevisiae | XX |
| 114 | 21 | 100.0 | 10 | 2 | AAW9684 | Aaw9684 Substance | DR |
| 115 | 21 | 100.0 | 10 | 2 | AAV06939 | Aay06939 Substance | XX |
| 116 | 21 | 100.0 | 10 | 2 | AAW26633 | Aaw92633 Human tac | PT |
| 117 | 21 | 100.0 | 10 | 4 | AAE66675 | Aab66675 Tachykinin | PT |
| 118 | 21 | 100.0 | 10 | 4 | AAK59347 | Aag9347 Atypical | XX |
| 119 | 21 | 100.0 | 10 | 4 | AAE6746 | Aag64746 Substance | PS |
| 120 | 21 | 100.0 | 10 | 4 | ADN12181 | Adn2181 Amino acid | XX |
| 121 | 21 | 100.0 | 10 | 8 | ADN27888 | Aon27888 Trichomonas | CC |
| 122 | 21 | 100.0 | 11 | 1 | AAE1480 | Aap61480 Sequence | CC |
| 123 | 21 | 100.0 | 11 | 1 | AAW80312 | Aap80312 Sequence | CC |
| 124 | 21 | 100.0 | 11 | 2 | AAK11854 | Aari1854 Undecapeptide | CC |
| 125 | 21 | 100.0 | 11 | 2 | AAK13162 | Aarl1362 Stalic acid | CC |
| 126 | 21 | 100.0 | 11 | 2 | AAK28442 | Aar28442 Substance | CC |
| 127 | 21 | 100.0 | 11 | 2 | AAK21969 | Aar21969 Cyclic bu | CC |
| 128 | 21 | 100.0 | 11 | 2 | AAK21942 | Aar21942 Substance | XX |
| 129 | 21 | 100.0 | 11 | 2 | AAK21962 | Aar21962 Substance | SQ |
| 130 | 21 | 100.0 | 11 | 2 | AAK21945 | Aar21945 Substance | Sequence 4 AA; |
| 131 | 21 | 100.0 | 11 | 2 | AAK21963 | Aar21963 Substance | Query Match 100.0%; Score 21; Length 4; |
| 132 | 21 | 100.0 | 11 | 2 | AAK21949 | Aar21949 Substance | ID AAY31075 standard; peptide; 4 AA. |
| 133 | 21 | 100.0 | 11 | 2 | AAK21951 | Aar21951 Substance | Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| 134 | 21 | 100.0 | 11 | 2 | AAK21954 | Aar21954 Substance | Oy 1 FGIM 4 |
| 135 | 21 | 100.0 | 11 | 2 | AAK21946 | Aar21946 Substance | Db 1 FGIM 4 |
| 136 | 21 | 100.0 | 11 | 2 | AAK21964 | Aar21964 Substance | |
| 137 | 21 | 100.0 | 11 | 2 | AAK21970 | Aar21970 Cyclic bu | |
| 138 | 21 | 100.0 | 11 | 2 | AAK21938 | Aar21938 Substance | |
| 139 | 21 | 100.0 | 11 | 2 | AAK21941 | Aar21941 Substance | |
| 140 | 21 | 100.0 | 11 | 2 | AAK21943 | Aar21943 Substance | RESULT 2 |
| 141 | 21 | 100.0 | 11 | 2 | AAK21954 | Aar21954 Substance | AAY31075 |
| 142 | 21 | 100.0 | 11 | 2 | AAK21946 | Aar21946 Neurokinin | ID AAY31075 standard; peptide; 4 AA. |
| 143 | 21 | 100.0 | 11 | 2 | AAK21964 | Aar85243 Substance | XX |
| 144 | 21 | 100.0 | 11 | 2 | AAK21970 | Aar77310 Substrate | AC AAY31075; |
| 145 | 21 | 100.0 | 11 | 2 | AAK21938 | Aar21938 Substance | XX |
| 146 | 21 | 100.0 | 11 | 2 | AAK219181 | Aar219181 Mono-Dipeptidyl Peptidase | XX |
| 147 | 21 | 100.0 | 11 | 2 | AAW3180 | Raw33180 Mono-Dipeptidyl Peptidase | DT 21-OCT-1999 (first entry) |
| 148 | 21 | 100.0 | 11 | 2 | AAW4616 | Raw04616 Substance | XX |
| 149 | 21 | 100.0 | 11 | 2 | AAW7975 | Raw7975 Substance | DB Non-crosslinked protein particle peptide 124. |
| 150 | 21 | 100.0 | 11 | 2 | AAW42973 | Raw42973 Substrate | XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse; albumin; haemoglobin; nanometer; micrometer; clearance. |
| | | | XX KW | | | OS Synthetic. | |
| | | | XX OS | | | SYNTHETIC. | |
| | | | XX PH | | | Location/Qualifiers | |
| | | | FT Key | | | | |
| | | | FT Modified-site | 4 | | /note= "C-terminal amide" | |
| | | | FT /note= | | | | |
| | | | XX XX | | | | |
| | | | XX PN | | | | |
| | | | XX US5945033-A. | | | | |
| | | | XX PD | | | | |
| | | | XX 31-AUG-1999. | | | | |
| | | | XX PP | | | | |
| | | | XX 12-NOV-1996; | | | | |
| | | | XX 96US-00747137. | | | | |
| | | | XX PR | | | | |
| | | | XX 15-JAN-1991; 91US-00641720. | | | | |
| | | | XX PR | | | | |
| | | | XX 13-OCT-1992; 92US-00959560. | | | | |
| | | | XX PR | | | | |
| | | | XX 01-JUN-1993; 93US-0068831. | | | | |
| | | | XX PR | | | | |
| | | | XX 14-MAR-1994; 94US-00212546. | | | | |
| | | | XX PA (HEMO-) HEMOSPHERE INC. | | | | |

ALIGNMENTS

| | | | | | | | |
|--|-------------|---------------|--------------------------|--|--|--|--|
| RESULT 1 | | | | | | | |
| AAW41683 | ID | AAW41683 | Standard; peptide; 4 AA. | | | | |
| XX AC | AC | AAW41683; | | | | | |
| XX DT | 09-JUN-1998 | (first entry) | | | | | |
| DE Peptide used in ophthalmic drug to treat corneal disorders. | | | | | | | |
| XX KW Ophthalmic drug; corneal disorder; ulcer; epithelial peeling; dry eye; keratitis; insulin like growth factor-I; IGF-I; eye drop. | | | | | | | |
| XX OS Synthetic. | | | | | | | |
| XX PH KEY | | | | | | | |
| Location/Qualifiers | | | | | | | |

105 12 57.1 9 2 Q7ZUJ3
106 12 57.1 9 2 Q7ZRJS
107 12 57.1 9 2 Q7ZRJ7
108 12 57.1 9 2 Q7ZRKL
109 12 57.1 10 1 C3U301 LOCMI
110 12 57.1 10 1 DYS5-LIMDU
111 12 57.1 10 1 DYS6-LIMSA
112 12 57.1 10 1 RT02-BOVIN
113 12 57.1 10 1 TK02-UREUN
114 12 57.1 10 2 Q7K059
115 12 57.1 10 2 Q25355
116 12 57.1 10 2 Q25356
117 12 57.1 10 2 Q85V65
118 12 57.1 10 2 Q85AC2
119 12 57.1 10 2 Q7MII1
120 12 57.1 10 2 Q9S05
121 12 57.1 10 2 Q8AE19
122 12 57.1 10 2 Q9R7JB
123 12 57.1 10 2 Q6LCTB
124 12 57.1 10 2 Q71VN2
125 12 57.1 10 2 Q83978
126 12 57.1 10 2 Q8JF67
127 12 57.1 10 2 Q8UJ33
128 12 57.1 11 1 PVKL-BLACK
129 12 57.1 11 1 PVKL-BLAUD
130 12 57.1 11 1 PVKL-GROPO
131 12 57.1 11 1 PVKL-LEUMA
132 12 57.1 11 1 PVKL-NAUCT
133 12 57.1 11 1 REA1-LITRU
134 12 57.1 11 2 Q9UQ46
135 12 57.1 11 2 Q6U255
136 12 57.1 11 2 Q7RH63
137 12 57.1 11 2 Q9TRX0
138 12 57.1 11 2 Q77871
139 12 57.1 11 2 Q77872
140 12 57.1 11 2 Q77873
141 12 57.1 11 2 Q34380
142 12 57.1 11 2 Q6RW4
143 12 57.1 11 2 Q7MIA0
144 12 57.1 11 2 Q7MIDI
145 12 57.1 11 2 Q8EU23
146 11 52.4 7 2 Q9C5B3
147 11 52.4 8 1 CALD-ENTPA
148 11 52.4 8 1 DYSS-LIMPA
149 11 52.4 8 1 DYSS-LIMSA
150 11 52.4 8 1 RT34-BOVIN

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secrete hormones, and contract (directly or indirectly) many smooth muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PROTEIN; PS00267; TACHYKININ; 1.
DR AMIDATION; Amphipathic defense peptide; Direct protein sequencing; Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RBS 11 1 Methionine amide.
SQ SEQUENCE 11 AA; 1294 MW; 3A2472CC981AB7 CRCE4;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

ALIGNMENTS

RESULT 1

| ID | TKN4_PSEGU | STANDARD: | PRT; | 11 AA. |
|----|---|-----------|------|--------|
| AC | PA42989; | | | |
| DT | 01-NOV-1995 (Rel. 32, Created) | | | |
| DT | 01-NOV-1995 (Rel. 32, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Substance P-like peptidase II (PG-SPII). | | | |
| OS | Pseudophryne guntheri (Quentiner's toadlet). | | | |
| OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae; Myobatrachinae; Pseudophryne. | | | |
| OC | "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri."; | | | |
| RT | Peptides 11:291-304 (1990). | | | |
| RC | TISSUE=Skin secretion; | | | |
| RX | MEDLINE=920287814; PubMed=2356157; DOI=10.1016/0166-9781(90)90086-K; | | | |
| RA | Simmaco M., Severini C., de Blasce D., Barra F., | | | |
| RA | Roberts J.D., Melchiorri P., Espanier V.; | | | |
| RT | "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri."; | | | |
| RL | PROTEIN; PS00267; TACHYKININ; 1. | | | |
| RC | AMIDATION; Amphipathic defense peptide; Direct protein sequencing; Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin. | | | |
| FT | MOD RES 1 1 Pyrrolidone carboxylic acid. | | | |
| FT | MOD RBS 11 1 Methionine amide. | | | |
| SQ | SEQUENCE 11 AA; 1293 MW; 3A2472CC981AB7 CRCE4; | | | |

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

RL Peptides 11:291-304 (1990).
 RC TISSUE=Skin secretion; MEDLINE=90087814; PubMed=2156157; DOI=10.1016/0166-9781(90)90086-K;
 RA Simmaco M., Severini C., de Blasce D., Barra F., Roberts J.D., Melchiorri P., Espanier V.;
 OC "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri.";
 OC Myobatrachinae; Pseudophryne.
 OC NCBI_TaxID=30349;
 RN [1]
 RP SQUENCE.

RL PROTEIN; PS00267; TACHYKININ; 1.

RC AMIDATION; Amphipathic defense peptide; Direct protein sequencing; Neuropeptide; Pyrrolidone carboxylic acid; Tachykinin.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.

FT MOD RBS 11 1 Methionine amide.

SQ SEQUENCE 11 AA; 1293 MW; 3A2472CC981AB7 CRCE4;

Query Match 100.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

GenCore version 5.1.6
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Om protein - protein search, using SW model

Run on: October 26, 2005, 08:12:37 ; Search time 20.4444 Seconds

(without alignments) 18.825 Million cell updates/sec

Title: US3910-053-669-2

Perfect score: 21
Sequence: 1 FGLM 4

Scoring table: BL0SUM62
Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum_DB_seq_length: 0
Maximum_DB_seq_length: 11

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database : PIR 79.0

Match 100%
List first 150 summaries

Total number of hits satisfying chosen parameters: 1328

Maximum_DB_seq_length: 11

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|---------------------|
| 1 | 21 | 100.0 | 11 | A60554 | substance P - guin |
| 2 | 21 | 100.0 | 11 | SPHO | substance P - hors |
| 3 | 21 | 100.0 | 11 | JN0023 | substance P - chick |
| 4 | 21 | 100.0 | 11 | S33300 | probable substance |
| 5 | 21 | 100.0 | 11 | E60409 | substance P-like P |
| 6 | 21 | 100.0 | 11 | F60409 | substance P-like P |
| 7 | 21 | 100.0 | 11 | S23308 | substance P - rain |
| 8 | 18 | 85.7 | 10 | B49581 | siyalokinin II - ye |
| 9 | 18 | 85.7 | 10 | A49581 | siyalokinin I - ye |
| 10 | 18 | 85.7 | 10 | A24867 | scyllokinin I - s |
| 11 | 18 | 85.7 | 10 | B61033 | rnatachaykinin B - |
| 12 | 18 | 85.7 | 11 | S07203 | uperolein - frog (|
| 13 | 18 | 85.7 | 11 | S07201 | physalaemin - frog |
| 14 | 18 | 85.7 | 11 | A61033 | rnatachaykinin A - |
| 15 | 16 | 76.2 | 8 | D4793 | neuropeptide calia |
| 16 | 16 | 76.2 | 10 | F60527 | sperm-activating p |
| 17 | 16 | 76.2 | 10 | B60589 | rnatachaykinin B - |
| 18 | 15 | 71.4 | 5 | PT0278 | Ig heavy chain CRD |
| 19 | 15 | 71.4 | 10 | SPPGK | neurokinin A - At1 |
| 20 | 15 | 71.4 | 10 | JN0024 | neurokinin K - pig |
| 21 | 15 | 71.4 | 10 | S06964 | neurokinin A - chi |
| 22 | 15 | 71.4 | 10 | S21296 | hypothetical prote |
| 23 | 15 | 71.4 | 10 | 2 | 16K protein - poll |
| 24 | 15 | 71.4 | 10 | 2 | neurokinin A - rai |
| 25 | 15 | 71.4 | 10 | 2 | neurokinin A - At1 |
| 26 | 15 | 71.4 | 10 | 2 | phylomedulin - tw |
| 27 | 15 | 71.4 | 10 | 2 | rnatachaykinin C - |
| 28 | 15 | 71.4 | 10 | 2 | neurokinin A-relat |
| 29 | 15 | 71.4 | 11 | 1 | eleodoin - musky |
| 30 | | | | | eleodoin - curled |
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| | Matches | 4; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|---|---------|--------|---------------|-------|------------|----|--------|----|------|----|
| RESULT 2 | | | | | | | | | | |
| SPHO | Qy | 1 | FGLM | 4 | | | | | | |
| substance P - horse | | | | | | | | | | |
| C;Species: Equus caballus (domestic horse) | Db | 8 | FGLM | 11 | | | | | | |
| C;Accession: A01558 | | | | | | | | | | |
| R;Studer, R.O.; Trzeciak, A.; Lergier, W. | | | | | | | | | | |
| Helv. Chim. Acta 56, 860-866, 1973 | | | | | | | | | | |
| A;Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm. | | | | | | | | | | |
| A;Reference number: A01558 | | | | | | | | | | |
| A;Accession: A01558 | | | | | | | | | | |
| A;Molecule type: protein | | | | | | | | | | |
| A;Residues: 1-11 <STR> | | | | | | | | | | |
| A;Cross-references: UNIPROT:P01290 | | | | | | | | | | |
| C;Superfamily: substance P precursor | | | | | | | | | | |
| C;Keywords: amidated carboxyl end; hormone | | | | | | | | | | |
| F;11/Modified site: amidated carboxyl end (Met) #status experimental | | | | | | | | | | |
| Query Match | | 100 %; | Score 21; | DB 1; | length 11; | | | | | |
| Best Local Similarity | | 100 %; | Pred. No. 19; | | | | | | | |
| Matches | | 0; | Mismatches | 0; | Indels | 0; | Gap | 0; | | |
| RESULT 3 | | | | | | | | | | |
| JN0023 | Qy | 1 | FGLM | 4 | | | | | | |
| Substance P - chicken | Db | 8 | FGLM | 11 | | | | | | |
| C;Species: Gallus gallus (chicken) | | | | | | | | | | |
| C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 | | | | | | | | | | |
| C;Accession: JN0023 | | | | | | | | | | |
| R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L. | | | | | | | | | | |
| Regul. Pept. 20, 171-180, 1988 | | | | | | | | | | |
| A;Title: Arg3-substance P and neurokinin A from chicken small intestine. | | | | | | | | | | |
| A;Reference number: JN0023; MUID:88204263; PMID:2452461 | | | | | | | | | | |
| A;Accession: JN0023 | | | | | | | | | | |
| A;Molecule type: protein | | | | | | | | | | |
| A;Residues: 1-11 <CON> | | | | | | | | | | |
| A;Cross-references: UNIPROT:P19850 | | | | | | | | | | |
| C;Superfamily: substance P precursor | | | | | | | | | | |
| C;Keywords: amidated carboxyl end; tachykinin | | | | | | | | | | |
| F;11/Modified site: amidated carboxyl end (Met) #status predicted | | | | | | | | | | |
| Query Match | | 100 %; | Score 21; | DB 2; | length 11; | | | | | |
| Best Local Similarity | | 100 %; | Pred. No. 19; | | | | | | | |
| Matches | | 0; | Mismatches | 0; | Indels | 0; | Gap | 0; | | |
| RESULT 4 | | | | | | | | | | |
| S33300 | Qy | 1 | FGLM | 4 | | | | | | |
| Probable substance P - smaller spotted catshark | Db | 8 | FGLM | 11 | | | | | | |
| C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish) | | | | | | | | | | |
| C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 | | | | | | | | | | |
| C;Accession: S33300 | | | | | | | | | | |
| R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M. | | | | | | | | | | |
| Bur, J. Biochem. 214, 469-474, 1993 | | | | | | | | | | |
| A;Title: Primary structures and biological activities of substance-P-related peptides frc | | | | | | | | | | |
| A;Reference number: S33300; MUID:93292508; PMID:7685693 | | | | | | | | | | |
| A;Accession: S33300 | | | | | | | | | | |
| A;Molecule type: protein | | | | | | | | | | |

ALIGNMENTS

N-acetylglycosamin

RESULT 1
A60654
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:9044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
R;Murphy, R.
A;Cross-reference: UNIPROT:P01290
C;Superfamily: substance
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

100 %;

Score 21;

DB 2;

length 11;

Best Local Similarity

100 %;

Pred. No. 19;

Matches

4;

Conservative

0;

Mismatches

0;

Indels

0;

Gap

0;

Best Local Similarity

100.0 %;

Score 21;

DB 1;

Length 11;

Best Local Similarity

100.0 %;

Pred. No. 19;

Length 11;

Best Local Similarity

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using BW model
Run on: October 26, 2005, 08:13:37 ; Search time 96.4444 Seconds
Title: US-10-053-669-2

Sequence: 21 FGLM 4
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510639 residues
Total number of hits satisfying chosen parameters: 250346

Minimum DB seq length: 0
Maximum DB seq length: 11

POST-processing: Minimum Match 0%
Listing first 150 summaries

Database : /publib/published/applications/AA/*
1: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep: *
2: /cgn2_6/ptodata/1/pubpaa/PCTC_NEW_PUB.pep: *
3: /cgn2_6/ptodata/1/pubpaa/us06_NEW_PUB.pep: *
4: /cgn2_6/ptodata/1/pubpaa/us06_PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pubpaa/us07_NEW_PUB.pep: *
6: /cgn2_6/ptodata/1/pubpaa/RCRTS_PUBCOMB.pep: *
7: /cgn2_6/ptodata/1/pubpaa/us08_NEW_PUB.pep: *
8: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep: *
9: /cgn2_6/ptodata/1/pubpaa/us09A_PUBCOMB.pep: *
10: /cgn2_6/ptodata/1/pubpaa/us09B_PUBCOMB.pep: *
11: /cgn2_6/ptodata/1/pubpaa/us09C_PUBCOMB.pep: *
12: /cgn2_6/ptodata/1/pubpaa/us09_NNEW_PUB.pep: *
13: /cgn2_6/ptodata/1/pubpaa/us10_PUBCOMB.pep: *
14: /cgn2_6/ptodata/1/pubpaa/us10B_PUBCOMB.pep: *
15: /cgn2_6/ptodata/1/pubpaa/us10C_PUBCOMB.pep: *
16: /cgn2_6/ptodata/1/pubpaa/us10D_PUBCOMB.pep: *
17: /cgn2_6/ptodata/1/pubpaa/us10E_PUBCOMB.pep: *
18: /cgn2_6/ptodata/1/pubpaa/us10_NNEW_PUB.pep: *
19: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB.pep: *
20: /cgn2_6/ptodata/1/pubpaa/us11_NEWPUB.pep: *
21: /cgn2_6/ptodata/1/pubpaa/us60_NNEW_PUB.pep: *
22: /cgn2_6/ptodata/1/pubpaa/us60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query | # | Length | DB ID | Description |
|------------|-------|-------|---|--------|-------------------|---------------------|
| 1 | 21 | 100.0 | 4 | 9 | US-09-265-690C-2 | Sequence 2, Appli |
| 2 | 21 | 100.0 | 4 | 14 | US-10-230-133-3 | Sequence 3, Appli |
| 3 | 21 | 100.0 | 4 | 14 | US-10-053-669-2 | Sequence 2, Appli |
| 4 | 21 | 100.0 | 4 | 16 | US-10-695-536-3 | Sequence 3, Appli |
| 5 | 21 | 100.0 | 4 | 16 | US-10-805-881-2 | Sequence 2, Appli |
| 6 | 21 | 100.0 | 4 | 17 | US-10-497-628-2 | Sequence 2, Appli |
| 7 | 21 | 100.0 | 4 | 19 | US-11-018-690-3 | Sequence 3, Appli |
| 8 | 21 | 100.0 | 4 | 20 | US-11-056-697-623 | Sequence 623, Appli |
| 9 | 21 | 100.0 | 5 | 9 | US-09-265-690C-1 | Sequence 1, Appli |
| 10 | 21 | 100.0 | 5 | 14 | US-10-053-669-1 | Sequence 1, Appli |
| 11 | 21 | 100.0 | 5 | 15 | US-10-134-187-3 | Sequence 3, Appli |

| | | | | | | |
|----|----|-------|----|----|-------------------|---------------------|
| 12 | 21 | 100.0 | 5 | 16 | US-10-688-741-3 | Sequence 3, Appli |
| 13 | 21 | 100.0 | 5 | 16 | US-10-346-737A-30 | Sequence 1, Appli |
| 14 | 21 | 100.0 | 5 | 16 | US-10-805-881-1 | Sequence 3, Appli |
| 15 | 21 | 100.0 | 5 | 16 | US-10-720-039-3 | Sequence 15, Appli |
| 16 | 21 | 100.0 | 5 | 17 | US-10-497-628-15 | Sequence 16, Appli |
| 17 | 21 | 100.0 | 5 | 17 | US-10-497-628-16 | Sequence 17, Appli |
| 18 | 21 | 100.0 | 5 | 17 | US-10-497-628-17 | Sequence 565, Appli |
| 19 | 21 | 100.0 | 5 | 20 | US-11-066-697-565 | Sequence 604, Appli |
| 20 | 21 | 100.0 | 5 | 20 | US-11-066-697-604 | Sequence 3, Appli |
| 21 | 21 | 100.0 | 6 | 14 | US-10-168-789A-38 | Sequence 14, Appli |
| 22 | 21 | 100.0 | 6 | 17 | US-10-497-628-14 | Sequence 4, Appli |
| 23 | 21 | 100.0 | 6 | 17 | US-10-776-330-4 | Sequence 566, Appli |
| 24 | 21 | 100.0 | 6 | 20 | US-11-066-697-566 | Sequence 595, Appli |
| 25 | 21 | 100.0 | 6 | 20 | US-11-066-697-595 | Sequence 597, Appli |
| 26 | 21 | 100.0 | 6 | 20 | US-11-066-697-597 | Sequence 601, Appli |
| 27 | 21 | 100.0 | 6 | 20 | US-11-066-697-601 | Sequence 110, Appli |
| 28 | 21 | 100.0 | 7 | 14 | US-10-036-542-111 | Sequence 111, Appli |
| 29 | 21 | 100.0 | 7 | 14 | US-10-036-542-111 | Sequence 37, Appli |
| 30 | 21 | 100.0 | 7 | 14 | US-10-168-789A-37 | Sequence 2, Appli |
| 31 | 21 | 100.0 | 7 | 15 | US-10-134-187-2 | Sequence 2, Appli |
| 32 | 21 | 100.0 | 7 | 16 | US-10-688-741-2 | Sequence 13, Appli |
| 33 | 21 | 100.0 | 7 | 16 | US-10-720-039-2 | Sequence 13, Appli |
| 34 | 21 | 100.0 | 7 | 17 | US-10-497-628-13 | Sequence 596, Appli |
| 35 | 21 | 100.0 | 7 | 20 | US-11-066-697-596 | Sequence 597, Appli |
| 36 | 21 | 100.0 | 7 | 20 | US-11-066-697-607 | Sequence 1, Appli |
| 37 | 21 | 100.0 | 7 | 20 | US-11-025-494-2 | Sequence 36, Appli |
| 38 | 21 | 100.0 | 8 | 14 | US-10-168-789A-36 | Sequence 1, Appli |
| 39 | 21 | 100.0 | 8 | 17 | US-10-497-628-12 | Sequence 583, Appli |
| 40 | 21 | 100.0 | 8 | 20 | US-11-066-697-583 | Sequence 592, Appli |
| 41 | 21 | 100.0 | 8 | 20 | US-11-066-697-592 | Sequence 600, Appli |
| 42 | 21 | 100.0 | 8 | 20 | US-11-066-697-600 | Sequence 112, Appli |
| 43 | 21 | 100.0 | 9 | 14 | US-10-036-542-112 | Sequence 35, Appli |
| 44 | 21 | 100.0 | 9 | 14 | US-10-168-789A-35 | Sequence 622, Appli |
| 45 | 21 | 100.0 | 9 | 15 | US-10-134-187-1 | Sequence 64, Appli |
| 46 | 21 | 100.0 | 9 | 15 | US-10-390-494-1 | Sequence 1, Appli |
| 47 | 21 | 100.0 | 9 | 16 | US-10-688-741-1 | Sequence 1, Appli |
| 48 | 21 | 100.0 | 9 | 16 | US-10-720-039-1 | Sequence 1, Appli |
| 49 | 21 | 100.0 | 9 | 16 | US-11-066-697-545 | Sequence 545, Appli |
| 50 | 21 | 100.0 | 9 | 20 | US-11-066-697-622 | Sequence 622, Appli |
| 51 | 21 | 100.0 | 9 | 20 | US-11-025-494-1 | Sequence 64, Appli |
| 52 | 21 | 100.0 | 9 | 21 | US-10-168-789A-34 | Sequence 34, Appli |
| 53 | 21 | 100.0 | 10 | 17 | US-10-451-304-1 | Sequence 1, Appli |
| 54 | 21 | 100.0 | 10 | 17 | US-11-066-697-621 | Sequence 621, Appli |
| 55 | 21 | 100.0 | 10 | 20 | US-11-066-697-621 | Sequence 71, Appli |
| 56 | 21 | 100.0 | 10 | 20 | US-11-066-697-621 | Sequence 3, Appli |
| 57 | 21 | 100.0 | 11 | 9 | US-09-205-690C-3 | Sequence 64, Appli |
| 58 | 21 | 100.0 | 11 | 9 | US-09-935-682-64 | Sequence 26, Appli |
| 59 | 21 | 100.0 | 11 | 9 | US-09-841-909B-26 | Sequence 1, Appli |
| 60 | 21 | 100.0 | 11 | 10 | US-09-988-792-1 | Sequence 1, Appli |
| 61 | 21 | 100.0 | 11 | 10 | US-09-988-792-6 | Sequence 1, Appli |
| 62 | 21 | 100.0 | 11 | 10 | US-09-988-792-8 | Sequence 7, Appli |
| 63 | 21 | 100.0 | 11 | 10 | US-09-988-792-10 | Sequence 8, Appli |
| 64 | 21 | 100.0 | 11 | 13 | US-10-002-533-4 | Sequence 10, Appli |
| 65 | 21 | 100.0 | 11 | 14 | US-10-230-133-1 | Sequence 4, Appli |
| 66 | 21 | 100.0 | 11 | 14 | US-10-053-669-3 | Sequence 1, Appli |
| 67 | 21 | 100.0 | 11 | 14 | US-10-111-934-3 | Sequence 3, Appli |
| 68 | 21 | 100.0 | 11 | 14 | US-10-114-833B-24 | Sequence 24, Appli |
| 69 | 21 | 100.0 | 11 | 14 | US-10-197-954-130 | Sequence 130, Appli |
| 70 | 21 | 100.0 | 11 | 14 | US-10-251-703-25 | Sequence 25, Appli |
| 71 | 21 | 100.0 | 11 | 14 | US-10-168-789A-17 | Sequence 17, Appli |
| 72 | 21 | 100.0 | 11 | 14 | US-10-423-714-4 | Sequence 4, Appli |
| 73 | 21 | 100.0 | 11 | 15 | US-10-343-634-27 | Sequence 27, Appli |
| 74 | 21 | 100.0 | 11 | 15 | US-10-289-009-24 | Sequence 24, Appli |
| 75 | 21 | 100.0 | 11 | 15 | US-10-289-009-25 | Sequence 25, Appli |
| 76 | 21 | 100.0 | 11 | 15 | US-10-289-009-26 | Sequence 26, Appli |
| 77 | 21 | 100.0 | 11 | 15 | US-10-167-637-65 | Sequence 65, Appli |
| 78 | 21 | 100.0 | 11 | 16 | US-10-695-636-1 | Sequence 1, Appli |
| 79 | 21 | 100.0 | 11 | 16 | US-10-805-881-3 | Sequence 3, Appli |
| 80 | 21 | 100.0 | 11 | 16 | US-10-805-881-3 | Sequence 4, Appli |
| 81 | 21 | 100.0 | 11 | 17 | US-10-813-886-4 | Sequence 130, Appli |
| 82 | 21 | 100.0 | 11 | 17 | US-10-760-895-130 | Sequence 13, Appli |
| 83 | 21 | 100.0 | 11 | 17 | US-10-839-017-13 | Sequence 1, Appli |
| 84 | 21 | 100.0 | 11 | 17 | US-10-768-974-1 | Sequence 1, Appli |

ALIGNMENTS

Om protein - protein search, using sw model

Run on: October 26, 2005, 08:17:28 ; Search time 27.111 Seconds
 (w/o alignment)
 11.014 Million cell updates/sec

Title: US-10-053-669-2

Searched: 21 FGLM 4

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB-seq length: 11

Post-processing: Minimum Match 0%
 Listing first 150 summaries

Database : Issued-Patents AA:*

1: /cgn2_6/pctdata/1/iaa/5A_COMB.pep: *
 2: /cgn2_6/pctdata/1/iaa/5B_COMB.pep: *
 3: /cgn2_6/pctdata/1/iaa/6A_COMB.pep: *
 4: /cgn2_6/pctdata/1/iaa/6B_COMB.pep: *
 5: /cgn2_6/pctdata/1/iaa/PCUS_COMB.pep: *
 6: /cgn2_6/pctdata/1/iaa/backfile1.pep: *

Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|--------------------|--------------------|
| 1 | 21 | 100.0 | 4 | 1 | US-08-441-591-63 | Sequence 63, Appl |
| 2 | 21 | 100.0 | 4 | 1 | US-08-303-362A-63 | Sequence 63, Appl |
| 3 | 21 | 100.0 | 4 | 3 | US-03-265-690C-2 | Sequence 2, Appl |
| 4 | 21 | 100.0 | 4 | 4 | US-03-265-263-3 | Sequence 3, Appl |
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| 6 | 21 | 100.0 | 4 | 5 | PCT-US95-05600-80 | Sequence 80, Appl |
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| 13 | 21 | 100.0 | 6 | 1 | US-08-428-692-41 | Sequence 3, Appl |
| 14 | 21 | 100.0 | 6 | 1 | US-07-712-828B-7 | Sequence 7, Appl |
| 15 | 21 | 100.0 | 6 | 1 | US-08-430-238-15 | Sequence 15, Appl |
| 16 | 21 | 100.0 | 6 | 2 | US-07-737-371B-5 | Sequence 5, Appl |
| 17 | 21 | 100.0 | 6 | 3 | US-09-317-125-5 | Sequence 48, Appl |
| 18 | 21 | 100.0 | 6 | 4 | US-09-428-692-39 | Sequence 1, Appl |
| 19 | 21 | 100.0 | 6 | 4 | US-08-428-692-41 | Sequence 3, Appl |
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| 21 | 21 | 100.0 | 7 | 2 | US-07-731-371B-8 | Sequence 8, Appl |
| 22 | 21 | 100.0 | 7 | 4 | US-09-428-692-42 | Sequence 5, Appl |
| 23 | 21 | 100.0 | 8 | 2 | US-07-737-371B-10 | Sequence 10, Appl |
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| 27 | 21 | 100.0 | 9 | 2 | US-08-293-284A-6 | Sequence 6, Appl |
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| 30 | 21 | 100.0 | 10 | 1 | US-08-437-820-6 | Sequence 6, Appl |
| 31 | 21 | 100.0 | 10 | 2 | US-07-731-371B-9 | Sequence 2, Appl |
| 32 | 21 | 100.0 | 10 | 3 | US-09-167-548-2 | Sequence 2, Appl |
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| 41 | 21 | 100.0 | 11 | 1 | US-08-428-488-15 | Sequence 15, Appl |
| 42 | 21 | 100.0 | 11 | 1 | US-08-391-910-2 | Sequence 2, Appl |
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| 56 | 21 | 100.0 | 11 | 1 | US-08-441-591-6 | Sequence 6, Appl |
| 57 | 21 | 100.0 | 11 | 1 | US-08-247-247A-1 | Sequence 1, Appl |
| 58 | 21 | 100.0 | 11 | 1 | US-08-464-248A-1 | Sequence 1, Appl |
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| 63 | 21 | 100.0 | 11 | 2 | US-08-441-591-11 | Sequence 1, Appl |
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| 65 | 21 | 100.0 | 11 | 2 | US-07-737-371B-16 | Sequence 16, Appl |
| 66 | 21 | 100.0 | 11 | 2 | US-07-731-371B-17 | Sequence 17, Appl |
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| 70 | 21 | 100.0 | 11 | 2 | US-07-737-371B-34 | Sequence 34, Appl |
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| 75 | 21 | 100.0 | 11 | 3 | US-08-891-157A-4 | Sequence 17, Appl |
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| 88 | 21 | 100.0 | 11 | 4 | US-09-428-692-21 | Sequence 1, Appl |
| 89 | 21 | 100.0 | 11 | 4 | US-09-285-387A-1 | Sequence 1, Appl |
| 90 | 21 | 100.0 | 11 | 5 | PCT-US92-06500-23 | Sequence 21, Appl |
| 91 | 21 | 100.0 | 11 | 5 | PCT-US95-05600-23 | Sequence 21, Appl |
| 92 | 21 | 100.0 | 11 | 6 | 5441935-1 | Patent No. 5441935 |
| 93 | 21 | 100.0 | 11 | 6 | 5441935-1 | Patent No. 5441935 |
| 94 | 18 | 85.7 | 8 | 3 | US-09-258-754-354 | Sequence 34, App |
| 95 | 18 | 85.7 | 8 | 3 | US-09-042-107-354 | Sequence 34, App |
| 96 | 18 | 85.7 | 8 | 4 | US-09-728-2500-354 | Sequence 34, App |
| 97 | 18 | 85.7 | 8 | 4 | US-09-676-472A-354 | Sequence 34, App |
| 98 | 18 | 85.7 | 10 | 3 | US-08-021-623C-2 | Sequence 2, Appl |
| 99 | 18 | 85.7 | 10 | 3 | US-08-293-728-17 | Sequence 17, Appl |
| 100 | 18 | 85.7 | 10 | 3 | US-09-421-868-17 | Sequence 17, Appl |

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| 101 | 18 | 85.7 | 11 | 1 | US-07-731-909B-2 | Sequence 2, Appli |
| 102 | 18 | 85.7 | 11 | 1 | US-08-428-488-16 | Sequence 16, Appli |
| 103 | 18 | 85.7 | 11 | 1 | US-08-220-789A-56 | Sequence 56, Appli |
| 104 | 18 | 85.7 | 11 | 2 | US-08-766-598-7 | Sequence 7, Appli |
| 105 | 18 | 85.7 | 11 | 2 | US-08-447-175A-7 | Sequence 7, Appli |
| 106 | 18 | 85.7 | 11 | 2 | US-07-731-371B-37 | Sequence 37, Appli |
| 107 | 18 | 85.7 | 11 | 3 | US-09-214-614-1 | Sequence 1, Appli |
| 108 | 18 | 85.7 | 11 | 4 | US-08-688-612-31 | Sequence 31, Appli |

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
ENTERING DATE:

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| 17 | 81.0 | 6 | 1 | US-08-486-006-78 | PRIOR CLASSIFICATION: | C435 |
| 17 | 81.0 | 6 | 2 | US-08-486-006-78 | PRIOR APPLICATION DATA: | |
| 17 | 81.0 | 8 | 3 | US-08-378-313-10 | APPLICATION NUMBER: | 08/303,362 |
| 10 | 81.0 | 10 | 2 | US-08-537-400-10 | FILING DATE: | 9-SEPTEMBER-1994 |
| 111 | 81.0 | 10 | 1 | US-08-747-137-124 | PRIOR APPLICATION DATA: | |
| 112 | 81.0 | 12 | 2 | US-08-722-126A-20 | APPLICATION NUMBER: | 07/714,131 |
| 113 | 81.0 | 4 | 3 | US-08-722-126A-20 | FILING DATE: | 10-JUNE-1991 |
| 114 | 81.0 | 4 | 3 | US-08-722-126A-20 | PRIOR APPLICATION DATA: | |
| 115 | 81.0 | 5 | 1 | US-08-739-184-163 | APPLICATION NUMBER: | 07/931,473 |
| 116 | 81.0 | 5 | 1 | US-08-522-320-17 | FILING DATE: | 17-AUGUST-1992 |
| 117 | 81.0 | 5 | 1 | US-08-475-265-163 | PRIOR APPLICATION DATA: | |
| 118 | 81.0 | 5 | 1 | US-08-435-886-163 | APPLICATION NUMBER: | 07/954,624 |
| 119 | 81.0 | 5 | 2 | US-08-477-362-163 | FILING DATE: | 8-SEPTEMBER-1993 |
| 120 | 81.0 | 5 | 2 | US-08-477-362-163 | PRIOR APPLICATION DATA: | |
| 121 | 81.0 | 5 | 2 | US-08-737-371B-47 | APPLICATION NUMBER: | 07/931,473 |
| 122 | 81.0 | 5 | 2 | US-08-737-371B-47 | FILING DATE: | 11-AUGUST-1990 |
| 123 | 81.0 | 5 | 3 | US-08-473-489A-163 | PRIOR APPLICATION DATA: | |
| 124 | 81.0 | 5 | 3 | US-08-435-693-163 | APPLICATION NUMBER: | 07/954,624 |
| 125 | 81.0 | 5 | 3 | US-08-476-163 | FILING DATE: | 21-OCTOBER-1992 |
| 126 | 81.0 | 5 | 4 | US-09-866-135A-2 | PRIOR APPLICATION DATA: | |
| 127 | 81.0 | 5 | 4 | US-10-337-103-3 | APPLICATION NUMBER: | 07/954,624 |
| 128 | 81.0 | 5 | 4 | US-10-337-103-3 | FILING DATE: | 21-OCTOBER-1992 |
| 129 | 81.0 | 6 | 3 | US-09-166-934-19 | PRIOR ATTORNEY/AGENT INFORMATION: | |
| 130 | 81.0 | 6 | 3 | US-09-166-934-19 | NAME: BATTI, J. Swanson | |
| 131 | 81.0 | 6 | 3 | US-07-822-273-3 | REGISTRATION NUMBER: | 33,215 |
| 132 | 81.0 | 6 | 7 | US-08-266-262-3 | REFERENCE/DOCKET NUMBER: | NEX21/ |
| 133 | 81.0 | 6 | 7 | US-08-286-262A-4 | TELECOMMUNICATION INFORMATION: | |
| 134 | 81.0 | 6 | 7 | US-08-548-974-12 | TELEPHONE: (303) 793-3333 | |
| 135 | 81.0 | 6 | 7 | US-09-830-428A-21 | TELEFAX: (303) 793-3433 | |
| 136 | 81.0 | 6 | 7 | US-09-214-450A-12 | INFORMATION FOR SEQ ID NO: 63: | |
| 137 | 81.0 | 6 | 7 | US-09-672-863-2 | SEQUENCE CHARACTERISTICS: | |
| 138 | 81.0 | 6 | 8 | US-08-522-326-4 | LENGTH: 4 | |
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| 141 | 81.0 | 6 | 8 | US-08-522-326-14 | TOPOLOGY: linear | |
| 142 | 81.0 | 6 | 8 | US-08-522-326-15 | US-08-441-591-63 | |
| 143 | 81.0 | 6 | 8 | US-08-714-053-6 | Query Match | |
| 144 | 81.0 | 6 | 8 | US-08-714-053-7 | Best Local Similarity | 100.0%; Pred |
| 145 | 81.0 | 6 | 8 | US-08-480-211-12 | Matches | 4; Conservative |
| 146 | 81.0 | 6 | 8 | US-09-421-211-12 | | |
| 147 | 81.0 | 6 | 8 | US-09-461-325-359 | | |
| 148 | 81.0 | 6 | 8 | US-10-012-542-359 | | |
| 149 | 81.0 | 6 | 8 | US-09-830-428A-14 | | |
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RESULT 2
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; Sequence 63, Application US/08303362P
; Patent No. 5648214
; GENERAL INFORMATION:

ALIGNMENTS

RESULT 1
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Sequence 63, Application US/08441591
; Patent No. 5637682
; GENERAL INFORMATION:
; APPLICANT: NIETUMLANDT, D., GOLD, L. AND WECU
; TITLE OF INVENTION: HIGH AFFINITY
; BROMONITROBENZYLIC ACID DERIVATIVES
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111

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(without alignment)
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Title:

Perfect score: 21
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Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:
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Post-processing: Minimum Match 0%
Listing first 150 summaries

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6: geneseq2003ab: *
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8: geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | |
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| 102 | 21 | 100.0 | 9 | 4 | AAB80325 | Human pro | PN | | | |
| 103 | 21 | 100.0 | 9 | 4 | AAB9146 | Tachykini | XX | | | |
| 104 | 21 | 100.0 | 9 | 4 | AAB91369 | Tachykini | PD | 31-DEC-1997. | | |
| 105 | 21 | 100.0 | 9 | 4 | AAG9348 | Atypical | XX | | | |
| 106 | 21 | 100.0 | 9 | 4 | AAB38833 | Membrane | PF | 11-JUN-1997; | 97WO-JP002015. | |
| 107 | 21 | 100.0 | 9 | 7 | ADF92328 | Substance | XX | | | |
| 108 | 21 | 100.0 | 9 | 8 | ADQ04477 | Substance | PR | 26-JUN-1996; | 96JP-00165612. | |
| 109 | 21 | 100.0 | 9 | 8 | ADN95076 | Mammalian | XX | | | |
| 110 | 21 | 100.0 | 9 | 8 | ADN15335 | Substance | PA | (SANT) SANTEN PHARM CO LTD. | | |
| 111 | 21 | 100.0 | 10 | 1 | AAP5033 | Substance | XX | | | |
| 112 | 21 | 100.0 | 10 | 2 | AAR21933 | Substance | PI | Nishida T, Nakamura M, Nakata K; | | |
| 113 | 21 | 100.0 | 10 | 4 | AAR65181 | S. cerevi | XX | | | |
| 114 | 21 | 100.0 | 10 | 2 | AAW99684 | Substance | DR | WPI; 1998-07607/07. | | |
| 115 | 21 | 100.0 | 10 | 2 | AAW06339 | AAW06339 | XX | | | |
| 116 | 21 | 100.0 | 10 | 2 | AAW92663 | Human tac | PT | Ophthalmic drug composition containing tetra:peptide - is useful as | | |
| 117 | 21 | 100.0 | 10 | 4 | AAB6675 | Tachykini | PT | corneal disorder remedy for corneal ulcer, corneal epithelial peeling, | | |
| 118 | 21 | 100.0 | 10 | 4 | AAB91445 | Tachykini | PT | dry eye, keratitis. | | |
| 119 | 21 | 100.0 | 10 | 4 | AAG99347 | Atypical | XX | | | |
| 120 | 21 | 100.0 | 10 | 4 | AAG64746 | Substance | PS | | | |
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| 122 | 21 | 100.0 | 10 | 8 | ADN27868 | Trichomon | CC | | | |
| 123 | 21 | 100.0 | 11 | 1 | AAP61480 | Sequence | CC | | | |
| 124 | 21 | 100.0 | 11 | 1 | AAP80312 | Sequence | CC | | | |
| 125 | 21 | 100.0 | 11 | 2 | AAR11854 | Undecapep | CC | | | |
| 126 | 21 | 100.0 | 11 | 2 | AAR13162 | Sialic ac | CC | | | |
| 127 | 21 | 100.0 | 11 | 2 | AAR28442 | Substance | CC | | | |
| 128 | 21 | 100.0 | 11 | 2 | AAR21969 | Cyclic su | CC | | | |
| 129 | 21 | 100.0 | 11 | 2 | AAR21942 | Substance | CC | 0.001-100 (preferably 0.01-10) mg/day of the tetrapeptide and | | |
| 130 | 21 | 100.0 | 11 | 2 | AAR21962 | Substance | XX | the composition is eye drops | | |
| 131 | 21 | 100.0 | 11 | 2 | AAR21945 | Substance | XX | | | |
| 132 | 21 | 100.0 | 11 | 2 | AAR21963 | Substance | SQ | | | |
| 133 | 21 | 100.0 | 11 | 2 | AAR21949 | Substance | | Sequence 4 AA; | | |
| 134 | 21 | 100.0 | 11 | 2 | AAR21951 | Substance | | | | |
| 135 | 21 | 100.0 | 11 | 2 | AAR21934 | Substance | | | | |
| 136 | 21 | 100.0 | 11 | 2 | AAR21946 | Substance | | | | |
| 137 | 21 | 100.0 | 11 | 2 | AAR21964 | Substance | | | | |
| 138 | 21 | 100.0 | 11 | 2 | AAR21970 | Cyclic su | | | | |
| 139 | 21 | 100.0 | 11 | 2 | AAR21938 | Substance | | | | |
| 140 | 21 | 100.0 | 11 | 2 | AAR21941 | Substance | | | | |
| 141 | 21 | 100.0 | 11 | 2 | AAR21943 | Substance | | | | |
| 142 | 21 | 100.0 | 11 | 2 | AAR21954 | Substance | | | | |
| 143 | 21 | 100.0 | 11 | 2 | AAR42646 | Substance | | | | |
| 144 | 21 | 100.0 | 11 | 2 | AAR85543 | Substance | | | | |
| 145 | 21 | 100.0 | 11 | 2 | AAR77310 | Substance | | | | |
| 146 | 21 | 100.0 | 11 | 2 | AAW33181 | AAW33181 Mono-DTPA | | | | |
| 147 | 21 | 100.0 | 11 | 2 | AAW33180 | AAW33180 Mono-DTPA | | | | |
| 148 | 21 | 100.0 | 11 | 2 | AAW04616 | Substance | | | | |
| 149 | 21 | 100.0 | 11 | 2 | AAW79775 | Substance | | | | |
| 150 | 21 | 100.0 | 11 | 2 | AAW2973 | Substrate | | | | |
| | | | | | | | | RESULT 2 | | |
| | | | | | | | | AYY31075 | | |
| | | | | | | | | ID AAY31075 standard; peptide; 4 AA. | | |
| | | | | | | | | Db 1 FGLM 4 | | |
| | | | | | | | | Ac AAY31075; | | |
| | | | | | | | | Dt 21-OCT-1999 (first entry) | | |
| | | | | | | | | XX Non-crosslinked protein particle peptide 124. | | |
| | | | | | | | | XX | | |

OM protein - protein search, using sw model
Run on: October 26, 2005, 08:36:48 ; Search time 170 Seconds
Copyright (c) 1993 - 2005 Compugen Ltd.

| | | | | | | | |
|-----|----|-------|----|---|------------|---------------------------|---|
| 105 | 22 | 100.0 | 87 | 2 | Q86U77 | Q86uu7 homo sapien | RC TISSUE=Brain; |
| 106 | 22 | 100.0 | 87 | 2 | Q6YMB9 | livilla com | RX MEDLINE=9329508; PubMed=7685693; |
| 107 | 22 | 100.0 | 87 | 2 | Q6YMC1 | livilla bae | RA Waugh D., Yang Y., Hazon N., Balment R.J., Conlon J.M.; |
| 108 | 22 | 100.0 | 87 | 2 | Q6YMC3 | livilla cap | RT "primary structures and biological activities of substance-p-related |
| 109 | 22 | 100.0 | 87 | 2 | Q6YMC9 | livilla mon | RT peptides from the brain of the dogfish, <i>Scyliorhinus canicula</i> ."; |
| 110 | 22 | 100.0 | 87 | 2 | Q6YMD1 | livilla mon | RT Bur. J. Blochem. 21:469-474 (1993). |
| 111 | 22 | 100.0 | 87 | 2 | Q6YMD3 | livilla mon | RL CC |
| 112 | 22 | 100.0 | 87 | 2 | Q6YMD5 | livilla mau | CC -!- FUNCTION: Tachykinins are active peptides which excite neurons, |
| 113 | 22 | 100.0 | 87 | 2 | Q6YMD7 | livilla bla | CC evoke behavioral responses, are potent vasodilators and |
| 114 | 22 | 100.0 | 87 | 2 | Q6YMD9 | livilla adu | CC secreteagogues, and contract (directly or indirectly) many smooth |
| 115 | 22 | 100.0 | 87 | 2 | Q6YME1 | Q9ymel | CC muscles. |
| 116 | 22 | 100.0 | 87 | 2 | Q6YME3 | cacophylla | CC -!- SUBCELLULAR LOCATION: Secreted. |
| 117 | 22 | 100.0 | 87 | 2 | Q6YMF3 | arycninis o | CC -!- SIMILARITY: Belongs to the tachykinin family. |
| 118 | 22 | 100.0 | 87 | 2 | Q6YMG7 | Q9ymg7 arcyainilla | DR PIR: A24867-A24867. |
| 119 | 22 | 100.0 | 87 | 2 | Q6YMH5 | Q5ymhs5 arcyainilla | DR InterPro: IPR02040; Tachy_Neurokinin. |
| 120 | 22 | 100.0 | 87 | 2 | Q6YMI3 | Q6ymj3 arcyainilla | DR PROSTIM; PS0267; TACHYKININ_1. |
| 121 | 22 | 100.0 | 87 | 2 | Q6YMJ9 | Q9ymj9 arcytininis | FT Amidation; Direct protein sequencing; Neuropeptide; Tachykinin. |
| 122 | 22 | 100.0 | 87 | 2 | Q6YMK1 | Q5ymn1 arcyainilla | FT MOD RSS 10 10 Methionine amide. |
| 123 | 22 | 100.0 | 87 | 2 | Q6YMN5 | Q6ymn5 arcyaina viri | FT SBOQUENCE 10 AA; 1219 MW; D0620B59c33AA9 CRC24; |
| 124 | 22 | 100.0 | 87 | 2 | Q6YMN7 | Q9ymn7 arcyaina ru | Db Query Match 100.0%; Score 22; DB 1; Length 10; |
| 125 | 22 | 100.0 | 87 | 2 | Q6YMQ3 | Q8ymq3 arcyaina ad | Db Best Local Similarity 80.0%; Pred. No. 1.4e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0; |
| 126 | 22 | 100.0 | 87 | 2 | Q6YMQ7 | Q9ymq7 arcyaina ad | Db Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0; |
| 127 | 22 | 100.0 | 87 | 2 | Q6YMQ9 | Q9ymq9 acizzia unc | Db |
| 128 | 22 | 100.0 | 87 | 2 | Q6YMR1 | P67377 mycobacteri | Db 1 FXGLM 5 |
| 129 | 22 | 100.0 | 87 | 2 | Q75YY3 | Q75yy3 euhadra qua | Db 6 FXGLM 10 |
| 130 | 22 | 100.0 | 89 | 2 | Q8LMB5 | Q91mb5 oryza sativa | Db |
| 131 | 22 | 100.0 | 92 | 1 | TKN2_OCTVU | Q816s2 octopus vul | Db |
| 132 | 22 | 100.0 | 92 | 2 | Q6ALI6 | Q9al16 desulfotile | Db |
| 133 | 22 | 100.0 | 93 | 1 | Y011_MYCRO | P67377 mycobacteri | Db |
| 134 | 22 | 100.0 | 93 | 1 | Y011_MYCTU | Q9al16 mycobacteri | Db |
| 135 | 22 | 100.0 | 93 | 1 | Y013_MYCLR | Q9al16 boletinellu | Db |
| 136 | 22 | 100.0 | 93 | 2 | Q6JZW7 | Q9185j | Db |
| 137 | 22 | 100.0 | 93 | 2 | Q71449 | Q9185j mycobacteri | Db |
| 138 | 22 | 100.0 | 94 | 2 | Q82PQ5 | Q92pq5 streptomyce | Db |
| 139 | 22 | 100.0 | 95 | 2 | Q9Y6T4 | Q9y6t4 homo sapien | Db |
| 140 | 22 | 100.0 | 96 | 1 | YNEC_ECO57 | P64462 escherichia | Db |
| 141 | 22 | 100.0 | 96 | 1 | YNEC_ECOL1 | P64461 escherichia | Db |
| 142 | 22 | 100.0 | 96 | 2 | Q86U78 | Q86uu8 homo sapien | Db |
| 143 | 22 | 100.0 | 96 | 2 | Q66EZ4 | Q86uu8 Q86ez4 yersinia ps | Db |
| 144 | 22 | 100.0 | 96 | 2 | Q74PWO | Q74pwo yersinia pe | Db |
| 145 | 22 | 100.0 | 96 | 2 | Q8ZIT1 | Q8zit1 yersinia pe | Db |
| 146 | 22 | 100.0 | 96 | 2 | Q83L16 | Q83l16 shigella fil | Db |
| 147 | 22 | 100.0 | 97 | 2 | Q8ND57 | Q9nd87 homo sapien | Db |
| 148 | 22 | 100.0 | 97 | 2 | Q6AB45 | Q6ab45 propionic acid | Db |
| 149 | 22 | 100.0 | 98 | 2 | Q7YCY0 | Q9ycyo sarcophaga | Db |
| 150 | 22 | 100.0 | 99 | 2 | Q9MLP9 | Q9mlp9 limulus pol | Db |

ALIGNMENTS

| RESULT 1 | TKN1_SKYCA | STANDARD; | PRT; | 10 AA. |
|----------|--|-----------|------|--------|
| AC | TKN1_SKYCA | | | |
| AC | P08608; | | | |
| DT | 01-AUG-1988 (Rel. 08, Created) | | | |
| DT | 01-AUG-1988 (Rel. 08, Last sequence update) | | | |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) | | | |
| DE | Scyliorhinus 1. | | | |
| OS | Scyliorhinus canicula (Spotted dogfish) (Spotted catshark) | | | |
| OC | Eukaryota; Metazoa; Chordata; Canisida; Vertebrata; Chondrichthyes; | | | |
| OC | Blasmodiaceae; Galeomorphi; Galeoidea; Carcarhiniiformes; | | | |
| OC | Scyliorhinidae; Scyliorhinus. | | | |
| OX | NCBI_TaxID:7830; | | | |
| RN | [1] | | | |
| RP | SEQUENCE. | | | |
| RC | TMSSUB=Intestine; PubMed=2422058; DOI=10.1016/0014-5793(86)900521-X; | | | |
| RX | Conlon J.M., Deacon C.P., O'Toole L., Thim L.; | | | |
| RT | Scyliorhinus I and II: two novel tachykinins from dogfish gut."; | | | |
| RL | FERS Lett. 200:111-116(1986); | | | |
| RN | [2] | | | |
| RP | SEQUENCE. | | | |
| RC | MEDLINE=86192829; PubMed=2422058; DOI=10.1016/0014-5793(86)900521-X; | | | |
| RX | Conlon J.M., Deacon C.P., O'Toole L., Thim L.; | | | |
| RT | Scyliorhinus I and II: two novel tachykinins from dogfish gut."; | | | |
| RL | FERS Lett. 200:111-116(1986); | | | |
| RN | [2] | | | |
| RP | SEQUENCE. | | | |
| RC | TMSSUB=Intestine; PubMed=2422058; DOI=10.1016/0014-5793(86)900521-X; | | | |
| RX | Conlon J.M., Deacon C.P., O'Toole L., Thim L.; | | | |
| RT | Scyliorhinus I and II: two novel tachykinins from dogfish gut."; | | | |
| RL | FERS Lett. 200:111-116(1986); | | | |
| RN | [2] | | | |
| RP | SEQUENCE. | | | |

| | |
|----|---|
| RC | TISSUE=Brain; |
| RX | RX MEDLINE=9329508; PubMed=7685693; |
| RA | RA Waugh D., Yang Y., Hazon N., Balment R.J., Conlon J.M.; |
| RT | RT "primary structures and biological activities of substance-p-related |
| RT | RT peptides from the brain of the dogfish, <i>Scyliorhinus canicula</i> ."; |
| RT | RT Bur. J. Blochem. 21:469-474 (1993). |
| RL | RL CC |
| CC | -!- FUNCTION: Tachykinins are active peptides which excite neurons, |
| CC | evoke behavioral responses, are potent vasodilators and |
| CC | secreteagogues, and contract (directly or indirectly) many smooth |
| CC | muscles. |
| CC | -!- SUBCELLULAR LOCATION: Secreted. |
| CC | -!- SIMILARITY: Belongs to the tachykinin family. |
| DR | DR PIR: A24867-A24867. |
| DR | DR InterPro: IPR02040; Tachy_Neurokinin. |
| DR | DR PROSTIM; PS0267; TACHYKININ_1. |
| FT | FT Amidation; Direct protein sequencing; Neuropeptide; Tachykinin. |
| FT | FT MOD RSS 10 10 Methionine amide. |
| FT | FT SBOQUENCE 10 AA; 1219 MW; D0620B59c33AA9 CRC24; |
| Db | Db Query Match 100.0%; Score 22; DB 1; Length 10; |
| Db | Db Best Local Similarity 80.0%; Pred. No. 1.4e+02; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0; |
| Db | Db Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0; |
| OY | OY 1 FXGLM 5 |
| Db | Db 6 FXGLM 10 |

| Query Match | | | | | | | | | |
|-----------------------|----|-------|---------|-------|--------|-------|--------------|--------|----------------------------|
| Best Local Similarity | | Score | | Pred. | | DB | | Length | |
| 4; | | 80.0% | | 22; | | 1; | | 10; | |
| Qy | Db | 1 | FXGIM 5 | | | | | | |
| Matchers | | | | | | | | | |
| 110 | 22 | 100.0 | 175 | 2 | T11452 | NADH2 | dehydrogenas | 100.0% | Score 22; DB 1; Length 10; |
| 111 | 22 | 100.0 | 175 | 2 | T11413 | NADH2 | dehydrogenas | 104 | NADH2 dehydrogenas |
| 112 | 22 | 100.0 | 175 | 2 | T11258 | NADH2 | dehydrogenas | 105 | NADH2 dehydrogenas |
| 113 | 22 | 100.0 | 175 | 2 | T11093 | NADH2 | dehydrogenas | 106 | NADH2 dehydrogenas |
| 114 | 22 | 100.0 | 175 | 2 | T11061 | NADH2 | dehydrogenas | 107 | NADH2 dehydrogenas |
| 115 | 22 | 100.0 | 176 | 2 | S02210 | NADH2 | dehydrogenas | 108 | NADH2 dehydrogenas |
| 116 | 22 | 100.0 | 178 | 2 | T48711 | NADH2 | dehydrogenas | 109 | NADH2 dehydrogenas |
| 117 | 22 | 100.0 | 180 | 2 | F87358 | NADH2 | dehydrogenas | 110 | NADH2 dehydrogenas |
| 118 | 22 | 100.0 | 181 | 2 | F81851 | NADH2 | dehydrogenas | 111 | NADH2 dehydrogenas |
| 119 | 22 | 100.0 | 184 | 2 | S74741 | NADH2 | dehydrogenas | 112 | NADH2 dehydrogenas |
| 120 | 22 | 100.0 | 184 | 2 | E90077 | NADH2 | dehydrogenas | 113 | NADH2 dehydrogenas |
| 121 | 22 | 100.0 | 187 | 2 | T02887 | NADH2 | dehydrogenas | 114 | NADH2 dehydrogenas |
| 122 | 22 | 100.0 | 187 | 2 | AF1870 | NADH2 | dehydrogenas | 115 | NADH2 dehydrogenas |
| 123 | 22 | 100.0 | 191 | 2 | AB2135 | NADH2 | dehydrogenas | 116 | NADH2 dehydrogenas |
| 124 | 22 | 100.0 | 193 | 2 | T26510 | NADH2 | dehydrogenas | 117 | NADH2 dehydrogenas |
| 125 | 22 | 100.0 | 195 | 2 | H98274 | NADH2 | dehydrogenas | 118 | NADH2 dehydrogenas |
| 126 | 22 | 100.0 | 197 | 2 | T36696 | NADH2 | dehydrogenas | 119 | NADH2 dehydrogenas |
| 127 | 22 | 100.0 | 198 | 2 | A34247 | NADH2 | dehydrogenas | 120 | NADH2 dehydrogenas |
| 128 | 22 | 100.0 | 199 | 2 | S73702 | NADH2 | dehydrogenas | 121 | NADH2 dehydrogenas |
| 129 | 22 | 100.0 | 200 | 1 | A39741 | NADH2 | dehydrogenas | 122 | NADH2 dehydrogenas |
| 130 | 22 | 100.0 | 203 | 2 | B90055 | NADH2 | dehydrogenas | 123 | NADH2 dehydrogenas |
| 131 | 22 | 100.0 | 205 | 2 | T08398 | NADH2 | dehydrogenas | 124 | NADH2 dehydrogenas |
| 132 | 22 | 100.0 | 208 | 2 | D97502 | NADH2 | dehydrogenas | 125 | NADH2 dehydrogenas |
| 133 | 22 | 100.0 | 210 | 2 | A34247 | NADH2 | dehydrogenas | 126 | NADH2 dehydrogenas |
| 134 | 22 | 100.0 | 210 | 2 | NH2720 | NADH2 | dehydrogenas | 127 | NADH2 dehydrogenas |
| 135 | 22 | 100.0 | 210 | 2 | T28002 | NADH2 | dehydrogenas | 128 | NADH2 dehydrogenas |
| 136 | 22 | 100.0 | 210 | 2 | AD2818 | NADH2 | dehydrogenas | 129 | NADH2 dehydrogenas |
| 137 | 22 | 100.0 | 211 | 1 | ICMS6 | NADH2 | dehydrogenas | 130 | NADH2 dehydrogenas |
| 138 | 22 | 100.0 | 211 | 2 | A34247 | NADH2 | dehydrogenas | 131 | NADH2 dehydrogenas |
| 139 | 22 | 100.0 | 211 | 2 | D69529 | NADH2 | dehydrogenas | 132 | NADH2 dehydrogenas |
| 140 | 22 | 100.0 | 215 | 2 | JXK244 | NADH2 | dehydrogenas | 133 | NADH2 dehydrogenas |
| 141 | 22 | 100.0 | 215 | 2 | S23432 | NADH2 | dehydrogenas | 134 | NADH2 dehydrogenas |
| 142 | 22 | 100.0 | 216 | 2 | A12635 | NADH2 | dehydrogenas | 135 | NADH2 dehydrogenas |
| 143 | 22 | 100.0 | 217 | 2 | D53216 | NADH2 | dehydrogenas | 136 | NADH2 dehydrogenas |
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| 145 | 22 | 100.0 | 220 | 2 | G72349 | NADH2 | dehydrogenas | 138 | NADH2 dehydrogenas |
| 146 | 22 | 100.0 | 220 | 2 | D82210 | NADH2 | dehydrogenas | 139 | NADH2 dehydrogenas |
| 147 | 22 | 100.0 | 223 | 2 | E90392 | NADH2 | dehydrogenas | 140 | NADH2 dehydrogenas |
| 148 | 22 | 100.0 | 228 | 2 | E86253 | NADH2 | dehydrogenas | 141 | NADH2 dehydrogenas |
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| 150 | 22 | 100.0 | 230 | 1 | H64634 | NADH2 | dehydrogenas | 143 | NADH2 dehydrogenas |

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Om protein - protein search, using SW model
Run on: October 26, 2005, 08:40:49 ; Search time 166 Second(s)

Title: Perfect score: US;10-053-669-4
Sequence: 1 FXGLM 5

Scoring table: Biostar62DX Gapext 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 150 summaries

Database: Published Applications AB:

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| 3: /cgn2_6/ptodata/1/pubpaas/US06_NEW_PUBCOMB.pep:* |
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| 10: /cgn2_6/ptodata/1/pubpaas/US09B_PUBCOMB.pep:* |
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| 19: /cgn2_6/ptodata/1/pubpaas/US11A_PUBCOMB.pep:* |
| 20: /cgn2_6/ptodata/1/pubpaas/US11C_PUBCOMB.pep:* |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
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| 1 | 22 | 100.0 | 5 9 US-09-265-690C-1 | Sequence 1, Appli |
| 2 | 22 | 100.0 | 5 9 US-09-265-690C-1 | Sequence 4, Appli |
| 3 | 22 | 100.0 | 5 14 US-10-220-133-4 | Sequence 4, Appli |
| 4 | 22 | 100.0 | 5 14 US-10-033-661-1 | Sequence 1, Appli |
| 5 | 22 | 100.0 | 5 14 US-10-053-661-4 | Sequence 4, Appli |
| 6 | 22 | 100.0 | 5 15 US-1-124-187-3 | Sequence 3, Appli |
| 7 | 22 | 100.0 | 5 16 US-10-088-741-3 | Sequence 3, Appli |
| 8 | 22 | 100.0 | 5 16 US-10-695-533-4 | Sequence 4, Appli |
| 9 | 22 | 100.0 | 5 16 US-10-805-881-1 | Sequence 1, Appli |
| 10 | 22 | 100.0 | 5 16 US-10-805-881-4 | Sequence 4, Appli |
| 11 | 22 | 100.0 | 5 16 US-10-805-881-3 | Sequence 3, Appli |
| 12 | 100.0 | 5 16 US-10-988-792-7 | Sequence 7, Appli | |

RESULT 1
US-09-265-690C-1

ALIGNMENTS

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Sequence 1, Application US/09265690C
Publication No. US20010051345A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265, 690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO: 1
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: AMIDATION
US-09-265, 690C-1

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Best Local Similarity 100.0%; Score 22; DB 9; Length 5;
Match 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 FXGLM 5

RESULT 2
US-09-265-690C-4
Sequence 4, Application US/09265690C
Publication No. US20010051345A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Mac
FILE REFERENCE: 1427001
CURRENT APPLICATION NUMBER: US/09/265, 690C
CURRENT FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO: 4
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)..(5)
OTHER INFORMATION: AMIDATION
NAME/KEY: VARIANT
LOCATION: (2)..(2)
OTHER INFORMATION: "X" may be either Phe or Val.
US-09-265-690C-4

Query 5 FXGLM 5
Best Local Similarity 100.0%; Score 22; DB 9; Length 5;
Match 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 FXGLM 5

RESULT 3
US-10-230-133-4
Sequence 4, Application US/10230133
Publication No. US2003040625A1
GENERAL INFORMATION:
APPLICANT: Wells, Ibert
TITLE OF INVENTION: Antagonists of the magnesium binding defect as therapy agents and methods for treatment of abnormal physiological states

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GenCore version 5.1.6
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Om protein - protein search, using BW model

Run on: October 26, 2005, 08:37:58 ; Search time 43 Seconds
 (without alignments)
 8.680 Million cell updates/sec

Title: US-10-053-669-4

Perfect score: 22
 Sequence: 1 FXGLM 5

Scoring table: BioSumbDX Gapop-10^-0 Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing first 150 summaries

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 3: /cgn2_6/ptodata/1/1aa/6A_COMBO.pep: *
 4: /cgn2_6/ptodata/1/1aa/6B_COMBO.pep: *
 5: /cgn2_6/ptodata/1/1aa/PCU5_COMBO.pep: *
 6: /cgn2_6/ptodata/1/1aa/backFiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-----------------------|--------------------|
| 1 | 22 | 100.0 | 5 1 US-07-753-909B-3 | Sequence 3, Appli |
| 2 | 22 | 100.0 | 5 1 US-07-934-553-2 | Sequence 2, Appli |
| 3 | 22 | 100.0 | 5 1 US-08-265-288-1 | Sequence 1, Appli |
| 4 | 22 | 100.0 | 5 1 US-08-225-474-2 | Sequence 2, Appli |
| 5 | 22 | 100.0 | 5 1 US-08-391-910-1 | Sequence 1, Appli |
| 6 | 22 | 100.0 | 5 1 US-08-410-994-1 | Sequence 1, Appli |
| 7 | 22 | 100.0 | 5 1 US-08-391-814-1 | Sequence 1, Appli |
| 8 | 22 | 100.0 | 5 1 US-08-411-591-61 | Sequence 1, Appli |
| 9 | 22 | 100.0 | 5 1 US-08-303-362A-61 | Sequence 61, Appli |
| 10 | 22 | 100.0 | 5 1 US-08-462-415-1 | Sequence 1, Appli |
| 11 | 22 | 100.0 | 5 1 US-08-463-874-4 | Sequence 3, Appli |
| 12 | 22 | 100.0 | 5 1 US-08-444-135-1 | Sequence 1, Appli |
| 13 | 22 | 100.0 | 5 1 US-08-318-391-1 | Sequence 1, Appli |
| 14 | 22 | 100.0 | 5 2 US-07-737-371B-6 | Sequence 61, Appli |
| 15 | 22 | 100.0 | 5 3 US-08-257-965-1 | Sequence 61, Appli |
| 16 | 22 | 100.0 | 5 3 US-08-265-690C-1 | Sequence 1, Appli |
| 17 | 22 | 100.0 | 5 3 US-09-263-690C-4 | Sequence 1, Appli |
| 18 | 22 | 100.0 | 5 4 US-08-153-847-1 | Sequence 1, Appli |
| 19 | 22 | 100.0 | 5 4 US-08-635-265-4 | Sequence 1, Appli |
| 20 | 22 | 100.0 | 5 4 US-10-230-133-4 | Sequence 1, Appli |
| 21 | 22 | 100.0 | 5 5 PCT-US95-05600-78 | Sequence 78, Appli |
| 22 | 22 | 100.0 | 6 1 US-07-934-553-3 | Sequence 1, Appli |
| 23 | 22 | 100.0 | 6 1 US-08-225-474-3 | Sequence 3, Appli |
| 24 | 22 | 100.0 | 6 1 US-08-430-238-15 | Sequence 15, Appli |
| 25 | 22 | 100.0 | 6 2 US-07-737-371B-5 | Sequence 5, Appli |
| 26 | 22 | 100.0 | 6 2 US-07-737-371B-5 | Sequence 52, Appli |
| 27 | 22 | 100.0 | 6 3 US-09-317-125-5 | Sequence 5, Appli |

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| 28 | 22 | 100.0 | 6 4 US-09-428-692-39 | Sequence 39, Appli |
| 29 | 22 | 100.0 | 6 4 US-09-428-692-41 | Sequence 41, Appli |
| 30 | 22 | 100.0 | 7 1 US-07-712-828B-7 | Sequence 7, Appli |
| 31 | 22 | 100.0 | 7 2 US-07-737-371B-8 | Sequence 8, Appli |
| 32 | 22 | 100.0 | 7 2 US-07-737-371B-51 | Sequence 51, Appli |
| 33 | 22 | 100.0 | 7 4 US-09-428-692-42 | Sequence 42, Appli |
| 34 | 22 | 100.0 | 8 2 US-07-737-371E-10 | Sequence 10, Appli |
| 35 | 22 | 100.0 | 8 2 US-07-737-371E-56 | Sequence 56, Appli |
| 36 | 22 | 100.0 | 8 3 US-08-925-002-36 | Sequence 36, Appli |
| 37 | 22 | 100.0 | 8 4 US-09-910-552-36 | Sequence 60, Appli |
| 38 | 22 | 100.0 | 9 2 US-07-737-371B-60 | Sequence 2, Appli |
| 39 | 22 | 100.0 | 10 1 US-07-899-205-2 | Sequence 3, Appli |
| 40 | 22 | 100.0 | 10 1 US-07-999-210-3 | Sequence 6, Appli |
| 41 | 22 | 100.0 | 10 1 US-08-322-322-6 | Sequence 1, Appli |
| 42 | 22 | 100.0 | 10 1 US-08-193-393-1 | Sequence 9, Appli |
| 43 | 22 | 100.0 | 10 1 US-08-184-935-9 | Sequence 10, Appli |
| 44 | 22 | 100.0 | 10 1 US-08-184-935-10 | Sequence 3, Appli |
| 45 | 22 | 100.0 | 10 1 US-08-269-288-3 | Sequence 4, Appli |
| 46 | 22 | 100.0 | 10 1 US-08-338-484-2 | Sequence 2, Appli |
| 47 | 22 | 100.0 | 10 1 US-08-338-484-3 | Sequence 3, Appli |
| 48 | 22 | 100.0 | 10 1 US-08-175-432-2 | Sequence 2, Appli |
| 49 | 22 | 100.0 | 10 1 US-08-175-432-3 | Sequence 3, Appli |
| 50 | 22 | 100.0 | 10 1 US-08-462-413-3 | Sequence 4, Appli |
| 51 | 22 | 100.0 | 10 1 US-08-462-413-4 | Sequence 5, Appli |
| 52 | 22 | 100.0 | 10 1 US-08-391-814-3 | Sequence 6, Appli |
| 53 | 22 | 100.0 | 10 1 US-08-391-910-3 | Sequence 7, Appli |
| 54 | 22 | 100.0 | 10 1 US-08-418-994-3 | Sequence 8, Appli |
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| 56 | 22 | 100.0 | 10 1 US-08-418-994-5 | Sequence 10, Appli |
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| 59 | 22 | 100.0 | 10 1 US-08-167-870-2 | Sequence 13, Appli |
| 60 | 22 | 100.0 | 10 1 US-08-167-870-3 | Sequence 14, Appli |
| 61 | 22 | 100.0 | 10 1 US-08-437-820-6 | Sequence 15, Appli |
| 62 | 22 | 100.0 | 10 1 US-08-462-415-3 | Sequence 16, Appli |
| 63 | 22 | 100.0 | 10 1 US-08-462-415-4 | Sequence 17, Appli |
| 64 | 22 | 100.0 | 10 1 US-08-463-874-3 | Sequence 18, Appli |
| 65 | 22 | 100.0 | 10 1 US-08-463-874-4 | Sequence 19, Appli |
| 66 | 22 | 100.0 | 10 1 US-08-318-391-3 | Sequence 20, Appli |
| 67 | 22 | 100.0 | 10 1 US-08-318-391-4 | Sequence 21, Appli |
| 68 | 22 | 100.0 | 10 2 US-08-496-118-2 | Sequence 22, Appli |
| 69 | 22 | 100.0 | 10 2 US-07-737-371B-9 | Sequence 23, Appli |
| 70 | 22 | 100.0 | 10 2 US-07-737-371E-42 | Sequence 24, Appli |
| 71 | 22 | 100.0 | 10 2 US-07-737-371E-43 | Sequence 25, Appli |
| 72 | 22 | 100.0 | 10 2 US-07-737-371E-44 | Sequence 26, Appli |
| 73 | 22 | 100.0 | 10 2 US-07-737-371E-74 | Sequence 27, Appli |
| 74 | 22 | 100.0 | 10 2 US-07-737-371E-75 | Sequence 28, Appli |
| 75 | 22 | 100.0 | 10 2 US-07-737-371E-75 | Sequence 29, Appli |
| 76 | 22 | 100.0 | 10 3 US-08-257-965-3 | Sequence 30, Appli |
| 77 | 22 | 100.0 | 10 3 US-08-257-966-4 | Sequence 31, Appli |
| 78 | 22 | 100.0 | 10 3 US-09-168-540-2 | Sequence 32, Appli |
| 79 | 22 | 100.0 | 10 3 US-09-174-216-8 | Sequence 33, Appli |
| 80 | 22 | 100.0 | 10 4 US-08-153-847-3 | Sequence 34, Appli |
| 81 | 22 | 100.0 | 10 4 US-08-153-847-4 | Sequence 35, Appli |
| 82 | 22 | 100.0 | 10 4 US-09-152-060-110 | Sequence 36, Appli |
| 83 | 22 | 100.0 | 10 4 US-09-152-060-110 | Sequence 37, Appli |
| 84 | 22 | 100.0 | 10 6 US-09-152-060-110 | Sequence 38, Appli |
| 85 | 22 | 100.0 | 11 1 US-07-753-909B-2 | Sequence 39, Appli |
| 86 | 22 | 100.0 | 11 1 US-07-753-909B-2 | Sequence 40, Appli |
| 87 | 22 | 100.0 | 11 1 US-07-94-553-1 | Sequence 41, Appli |
| 88 | 22 | 100.0 | 11 1 US-08-184-935-12 | Sequence 42, Appli |
| 89 | 22 | 100.0 | 11 1 US-08-269-288-2 | Sequence 43, Appli |
| 90 | 22 | 100.0 | 11 1 US-08-338-484-1 | Sequence 44, Appli |
| 91 | 22 | 100.0 | 11 1 US-08-175-432-1 | Sequence 45, Appli |
| 92 | 22 | 100.0 | 11 1 US-08-462-413-2 | Sequence 46, Appli |
| 93 | 22 | 100.0 | 11 1 US-08-245-474-1 | Sequence 47, Appli |
| 94 | 22 | 100.0 | 11 1 US-08-418-994-2 | Sequence 48, Appli |
| 95 | 22 | 100.0 | 11 1 US-08-418-994-3 | Sequence 49, Appli |
| 96 | 22 | 100.0 | 11 1 US-08-300-503-3 | Sequence 50, Appli |
| 97 | 22 | 100.0 | 11 1 US-08-391-847-4 | Sequence 51, Appli |
| 98 | 22 | 100.0 | 11 1 US-08-157-870-1 | Sequence 52, Appli |
| 99 | 22 | 100.0 | 11 1 US-08-428-488-15 | Sequence 53, Appli |
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| 28 | 22 | 100.0 | 6 4 US-09-428-692-39 | Sequence 39, Appli |
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| 30 | 22 | 100.0 | 7 1 US-07-712-828B-7 | Sequence 7, Appli |
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| 32 | 22 | 100.0 | 7 2 US-07-737-371E-51 | Sequence 51, Appli |
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| 34 | 22 | 100.0 | 8 2 US-07-737-371E-10 | Sequence 10, Appli |
| 35 | 22 | 100.0 | 8 2 US-07-737-371E-56 | Sequence 56, Appli |
| 36 | 22 | 100.0 | 8 3 US-08-925-002-36 | Sequence 36, Appli |
| 37 | 22 | 100.0 | 8 4 US-09-910-552-36 | Sequence 36, Appli |
| 38 | 22 | 100.0 | 9 2 US-07-737-371E-60 | Sequence 60, Appli |
| 39 | 22 | 100.0 | 10 1 US-07-899-205-2 | Sequence 2, Appli |
| 40 | 22 | 100.0 | 10 1 US-07-999-210-3 | Sequence 3, Appli |
| 41 | 22 | 100.0 | 10 1 US-08-322-322-6 | Sequence 6, Appli |
| 42 | 22 | 100.0 | 10 1 US-08-193-393-1 | Sequence 1, Appli |
| 43 | 22 | 100.0 | 10 1 US-08-184-935-9 | Sequence 9, Appli |
| 44 | 22 | 100.0 | 10 1 US-08-184-935-10 | Sequence 10, Appli |
| 45 | 22 | 100.0 | 10 1 US-08-269-288-3 | Sequence 3, Appli |
| 46 | 22 | 100.0 | 10 1 US-08-338-484-2 | Sequence 2, Appli |
| 47 | 22 | 100.0 | 10 1 US-08-175-432-2 | Sequence 4, Appli |
| 48 | 22 | 100.0 | 10 1 US-08-462-413-2 | Sequence 5, Appli |
| 49 | 22 | 100.0 | 10 1 US-08-245-474-1 | Sequence 6, Appli |
| 50 | 22 | 100.0 | 10 1 US-08-418-994-2 | Sequence 7, Appli |
| 51 | 22 | 100.0 | 10 1 US-08-300-503-3 | Sequence 8, Appli |
| 52 | 22 | 100.0 | 10 1 US-08-391-847-4 | Sequence 9, Appli |
| 53 | 22 | 100.0 | 10 1 US-08-157-870-1 | Sequence 10, Appli |
| 54 | 22 | 100.0 | 10 1 US-08-428-488-15 | Sequence 11, Appli |
| 55 | 22 | 100.0 | 10 1 US-08-428-488-16 | Sequence 12, Appli |
| 56 | 22 | 100.0 | 10 1 US-08-428-488-17 | Sequence 13, Appli |
| 57 | 22 | 100.0 | 10 1 US-08-428-488-18 | Sequence 14, Appli |
| 58 | 22 | 100.0 | 10 1 US-08-428-488-19 | Sequence 15, Appli |
| 59 | 22 | 100.0 | 10 1 US-08-428-488-20 | Sequence 16, Appli |
| 60 | 22 | 100.0 | 10 1 US-08-428-488-21 | Sequence 17, Appli |
| 61 | 22 | 100.0 | 10 1 US-08-428-488-22 | Sequence 18, Appli |
| 62 | 22 | 100.0 | 10 1 US-08-428-488-23 | Sequence 19, Appli |
| 63 | 22 | 100.0 | 10 1 US-08-428-488-24 | Sequence 20, Appli |
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| 65 | 22 | 100.0 | 10 1 US-08-428-488-26 | Sequence 22, Appli |
| 66 | 22 | 100.0 | 10 1 US-08-428-488-27 | Sequence 23, Appli |
| 67 | 22 | 100.0 | 10 1 US-08-428-488-28 | Sequence 24, Appli |
| 68 | 22 | 100.0 | 10 1 US-08-428-488-29 | Sequence 25, Appli |
| 69 | 22 | 100.0 | 10 1 US-08-428-488-30 | Sequence 26, Appli |
| 70 | 22 | 100.0 | 10 1 US-08-428-488-31 | Sequence 27, Appli |
| 71 | 22 | 100.0 | 10 1 US-08-428-488-32 | Sequence 28, Appli |
| 72 | 22 | 100.0 | 10 1 US-08-428-488-33 | Sequence 29, Appli |
| 73 | 22 | 100.0 | 10 1 US-08-428-488-34 | Sequence 30, Appli |
| 74 | 22 | 100.0 | 10 1 US-08-428-488-35 | Sequence 31, Appli |
| 75 | 22 | 100.0 | 10 1 US-08-428-488-36 | Sequence 32, Appli |
| 76 | 22 | 100.0 | 10 1 US-08-428-488-37 | Sequence 33, Appli |
| 77 | 22 | 100.0 | 10 1 US-08-428-488-38 | Sequence 34, Appli |
| 78 | 22 | 100.0 | 10 1 US-08-428-488-39 | |

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/753,909B
 FILING DATE: 1993/09/03
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: FR 9106759
 FILING DATE: 04-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Sease, Edmund J.
 REGISTRATION NUMBER: 24,741
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (515)-288-3667
 FAX: (515)-288-1338
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: C-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rana ridibunda
 DEVELOPMENTAL STAGE: adult
 TISSUE TYPE: brain
 US-07-753-909B-3

Query Match 100.0%; Score 22; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gap 0;

OY 1 |||||
 Db 1 FXGLM 5

RESULT 2
 Sequence 2, Application US/07934553
 US-07-934-553-2
 Sequence 1, Appli
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 Sequence 150, Appli

ALIGNMENTS

RESULT 1
 US-07-753-909B-3
 ; Sequence 3, Application US/07753909B
 ; PATENT NO. 530632
 ; GENERAL INFORMATION:
 ; APPLICANT: Vaudry, Hubert
 ; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Zarley, McKee, Thome, Voorhees, and Sease
 ; STREET: 801 Grand, Suite 3200
 ; CITY: Des Moines
 ; STATE: Iowa
 ; COUNTRY: United States
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/934,553
 FILING DATE: 1993/08/21
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/705,071
 FILING DATE: 24-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Fentress, Susan B
 REGISTRATION NUMBER: 31,327
 REFERENCE/DOCKET NUMBER: NU-9033CIP
 TELECOMMUNICATION INFORMATION:

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Om protein - protein search, using SW model

Run on:

October 26, 2005, 08:34:00 ; Search time 165 Seconds

(without alignments)
11.720 Million cell updates/sec

Title: US-10-053-669-4
 Perfect score: 22
 Sequence: 1 PXGLM 5
 Scoring table: BioSIS(62DW)
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 38676381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB-seq-length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 150 summaries

Database :

1: geneseq 16Dec04:/*
 2: geneseqP1990B:/*
 3: geneseqP2000B:/*
 4: geneseqP2018:/*
 5: geneseqP2002B:/*
 6: geneseqP2003B:/*
 7: geneseqP2003bs:/*
 8: geneseqP2004B:/*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|---------------------------|
| 1 | 22 | 100.0 | 5 2 | AAR33009 |
| 2 | 22 | 100.0 | 5 2 | AAR33008 Alpha-subunit |
| 3 | 22 | 100.0 | 5 2 | AAR33007 Alpha-subunit |
| 4 | 22 | 100.0 | 5 2 | AAR33010 Alpha-subunit |
| 5 | 22 | 100.0 | 5 2 | AAR80134 COOH-terminal |
| 6 | 22 | 100.0 | 5 2 | AAR54549 Cholecystokinase |
| 7 | 22 | 100.0 | 5 2 | AAR54551 Cholecystokinase |
| 8 | 22 | 100.0 | 5 2 | AAR54550 Cholecystokinase |
| 9 | 22 | 100.0 | 5 2 | AAR54548 Cholecystokinase |
| 10 | 22 | 100.0 | 5 2 | AAR41687 Tetrapetide |
| 11 | 22 | 100.0 | 5 2 | AARW9643 Substance |
| 12 | 22 | 100.0 | 5 2 | AAY50325 Neutrophilin |
| 13 | 22 | 100.0 | 5 2 | AARW92660 Human tac |
| 14 | 22 | 100.0 | 5 3 | AAR23028 Mammalian |
| 15 | 22 | 100.0 | 5 3 | AAB23025 Human/rat |
| 16 | 22 | 100.0 | 5 3 | AAY67576 P antagonist |
| 17 | 22 | 100.0 | 5 4 | AAB66674 C-terminal |
| 18 | 22 | 100.0 | 5 4 | AAB82430 Fluorinat |
| 19 | 22 | 100.0 | 5 4 | AAB82431 Fluorinat |
| 20 | 22 | 100.0 | 5 4 | AAB911428 Tachykinin |
| 21 | 22 | 100.0 | 5 5 | AAB70556 Octopus |
| 22 | 22 | 100.0 | 5 5 | AAU10880 Human beta |
| 23 | 22 | 100.0 | 5 5 | AAB10088 Substance |
| 24 | 22 | 100.0 | 5 5 | AAU77847 Tachykinin |
| 25 | 22 | 100.0 | 5 5 | AAU77845 Tachykinin |

| | | | | | | |
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| 26 | 22 | 22 | 100.0 | 5 | 7 | ADCE4400 |
| 27 | 22 | 22 | 100.0 | 5 | 7 | ADFG9203 |
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| 29 | 22 | 22 | 100.0 | 5 | 8 | ADN12180 |
| 30 | 22 | 22 | 100.0 | 5 | 8 | ADN5078 |
| 31 | 22 | 22 | 100.0 | 5 | 8 | ADR43774 |
| 32 | 22 | 22 | 100.0 | 5 | 8 | ADR3771 |
| 33 | 22 | 22 | 100.0 | 6 | 1 | APB30443 |
| 34 | 22 | 22 | 100.0 | 6 | 1 | APB0519 |
| 35 | 22 | 22 | 100.0 | 6 | 1 | APB0694 |
| 36 | 22 | 22 | 100.0 | 6 | 1 | APB5032 |
| 37 | 22 | 22 | 100.0 | 6 | 1 | APB1486 |
| 38 | 22 | 22 | 100.0 | 6 | 2 | AAR07897 |
| 39 | 22 | 22 | 100.0 | 6 | 2 | AAR07893 |
| 40 | 22 | 22 | 100.0 | 6 | 2 | AAR21959 |
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| 45 | 22 | 22 | 100.0 | 6 | 2 | AAR26599 |
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| 56 | 22 | 22 | 100.0 | 6 | 4 | AABP086 |
| 57 | 22 | 22 | 100.0 | 6 | 4 | AAY0324 |
| 58 | 22 | 22 | 100.0 | 7 | 1 | ADE94202 |
| 59 | 22 | 22 | 100.0 | 7 | 1 | ADEP0310 |
| 60 | 22 | 22 | 100.0 | 7 | 2 | ARR195 |
| 61 | 22 | 22 | 100.0 | 7 | 2 | ARR21957 |
| 62 | 22 | 22 | 100.0 | 7 | 2 | AWB0086 |
| 63 | 22 | 22 | 100.0 | 7 | 2 | AWB2662 |
| 64 | 22 | 22 | 100.0 | 7 | 2 | AWB2705 |
| 65 | 22 | 22 | 100.0 | 7 | 3 | AAY67574 |
| 66 | 22 | 22 | 100.0 | 7 | 4 | ABP0323 |
| 67 | 22 | 22 | 100.0 | 7 | 4 | AGB9350 |
| 68 | 22 | 22 | 100.0 | 7 | 4 | ABR82428 |
| 69 | 22 | 22 | 100.0 | 7 | 4 | ABR8845 |
| 70 | 22 | 22 | 100.0 | 7 | 4 | ABR2429 |
| 71 | 22 | 22 | 100.0 | 7 | 4 | ABR91354 |
| 72 | 22 | 22 | 100.0 | 7 | 4 | ABR91431 |
| 73 | 22 | 22 | 100.0 | 7 | 4 | ABV1420 |
| 74 | 22 | 22 | 100.0 | 7 | 4 | ABV9350 |
| 75 | 22 | 22 | 100.0 | 7 | 5 | ABB0085 |
| 76 | 22 | 22 | 100.0 | 7 | 5 | ABB0085 |
| 77 | 22 | 22 | 100.0 | 7 | 7 | ADE94201 |
| 78 | 22 | 22 | 100.0 | 7 | 7 | ADF52529 |
| 79 | 22 | 22 | 100.0 | 7 | 8 | ADN5077 |
| 80 | 22 | 22 | 100.0 | 8 | 1 | APB20303 |
| 81 | 22 | 22 | 100.0 | 8 | 2 | APB844 |
| 82 | 22 | 22 | 100.0 | 8 | 2 | APB95950 |
| 83 | 22 | 22 | 100.0 | 8 | 2 | APW2664 |
| 84 | 22 | 22 | 100.0 | 8 | 2 | AWB27110 |
| 85 | 22 | 22 | 100.0 | 8 | 3 | AYG6753 |
| 86 | 22 | 22 | 100.0 | 8 | 4 | ABP1407 |
| 87 | 22 | 22 | 100.0 | 8 | 4 | ABP1416 |
| 88 | 22 | 22 | 100.0 | 8 | 4 | ABP1424 |
| 89 | 22 | 22 | 100.0 | 8 | 4 | AGB9349 |
| 90 | 22 | 22 | 100.0 | 8 | 4 | ABP9571 |
| 91 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 92 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 93 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 94 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 95 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 96 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 97 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |
| 98 | 22 | 22 | 100.0 | 8 | 5 | ABP09499 |

| | | | | | | | | | |
|-----|----|-------|----|---|----------|---|--|--|---------------------|
| 99 | 22 | 100.0 | 8 | 7 | ADD94200 | Ade94200 High acti hap5031 Substance | FT FT FT FT FT FT XX | Key Modified-site 4 /note= "alpha-Me-Leu" | Location/Qualifiers |
| 100 | 22 | 100.0 | 9 | 1 | AAR50314 | Aaw2714 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 101 | 22 | 100.0 | 9 | 2 | AAR27114 | Aab80325 Human pro | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 102 | 22 | 100.0 | 9 | 4 | AAB80325 | Aab91446 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 103 | 22 | 100.0 | 9 | 4 | AAB80325 | Aab91369 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 104 | 22 | 100.0 | 9 | 4 | AAB80325 | Aag99348 Atypical Substance | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 105 | 22 | 100.0 | 9 | 7 | ADD95076 | Adf92528 Substanc | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 106 | 22 | 100.0 | 9 | 8 | ADD95076 | Adn95076 Mammalin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 107 | 22 | 100.0 | 10 | 1 | AAP40414 | Aap40414 Decapepti | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 108 | 22 | 100.0 | 10 | 1 | AAP40414 | Aap40413 Decapepti | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 109 | 22 | 100.0 | 10 | 1 | AAP50633 | Aap50633 Substance | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 110 | 22 | 100.0 | 10 | 1 | AAP50633 | Aar21933 Substance | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 111 | 22 | 100.0 | 10 | 2 | AAR21933 | Aar65181 S. cerevi | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 112 | 22 | 100.0 | 10 | 2 | AAR21933 | Aar77311 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 113 | 22 | 100.0 | 10 | 2 | AAR21933 | Aar77312 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 114 | 22 | 100.0 | 10 | 2 | AAR21933 | Aar79777 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 115 | 22 | 100.0 | 10 | 2 | AAR21933 | Aar79776 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 116 | 22 | 100.0 | 10 | 2 | AAR21933 | Aaw48931 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 117 | 22 | 100.0 | 10 | 2 | AAR21933 | Aaw75251 Fragment | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 118 | 22 | 100.0 | 10 | 2 | AAN7415 | Ahw7415 HPMQ91 P | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 119 | 22 | 100.0 | 10 | 2 | AAY23264 | Aay23264 Protein b | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 120 | 22 | 100.0 | 10 | 2 | AAY6939 | Aay6939 Substance | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 121 | 22 | 100.0 | 10 | 2 | AAY6939 | Aaw2663 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 122 | 22 | 100.0 | 10 | 2 | AAY6939 | Aaw2663 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 123 | 22 | 100.0 | 10 | 2 | AAY6939 | Aaw26637 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 124 | 22 | 100.0 | 10 | 2 | AAY6939 | Aaw26689 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 125 | 22 | 100.0 | 10 | 2 | AAY6939 | Aaw92729 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 126 | 22 | 100.0 | 10 | 2 | AAY6939 | Aaw92728 Human tac | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 127 | 22 | 100.0 | 10 | 2 | AAY6939 | Aab82117 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 128 | 22 | 100.0 | 10 | 4 | AAB82417 | Aab91383 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 129 | 22 | 100.0 | 10 | 4 | AAB91383 | Aab91398 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 130 | 22 | 100.0 | 10 | 4 | AAB91383 | Aab91398 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 131 | 22 | 100.0 | 10 | 4 | AAB91383 | Aab91398 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 132 | 22 | 100.0 | 10 | 4 | AAB91383 | Aab91397 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 133 | 22 | 100.0 | 10 | 4 | AAB91383 | Aab91397 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 134 | 22 | 100.0 | 10 | 4 | AAB91383 | Aab91398 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 135 | 22 | 100.0 | 10 | 4 | AAB91445 | Aab91445 Tachykinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 136 | 22 | 100.0 | 10 | 4 | AAB99355 | Aab99355 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 137 | 22 | 100.0 | 10 | 4 | AAB99355 | Aab99355 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 138 | 22 | 100.0 | 10 | 4 | AAC99347 | Aac99347 Atypical Substance | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 139 | 22 | 100.0 | 10 | 4 | AAC99347 | Aag6746 Atypical Substance | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 140 | 22 | 100.0 | 10 | 4 | AAC99347 | Aab82381 Human neu | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 141 | 22 | 100.0 | 10 | 5 | AAB27117 | Aae27017 Human gen | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 142 | 22 | 100.0 | 10 | 5 | AAB27117 | Aae27155 Human gen | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 143 | 22 | 100.0 | 10 | 5 | AAB27117 | Aab99004 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 144 | 22 | 100.0 | 10 | 5 | AAB27117 | Aab99004 Neurokinin | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 145 | 22 | 100.0 | 10 | 6 | ABP76074 | Abg76074 Sea lampr | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 146 | 22 | 100.0 | 10 | 6 | ABP76074 | Abg65038 Human sec | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 147 | 22 | 100.0 | 10 | 6 | ABP76074 | Abg65038 Human sec | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 148 | 22 | 100.0 | 10 | 7 | ADG63998 | Adc63998 Mosquito | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 149 | 22 | 100.0 | 10 | 7 | ADG63998 | Adc63998 Mosquito | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |
| 150 | 22 | 100.0 | 10 | 8 | ADG89837 | Adg89837 Human sec | FT FT FT FT FT FT XX | Key Modified-site 5 /note= "Met-NH2" | Location/Qualifiers |

ALIGNMENTS

RESULT 1
 AAR33009 ID AAR33009 Standard; peptide: 5 AA.
 AC AAR33009;
 XX DT 25-MAR-2003 (revised)
 DT 02-APR-1993 (first entry)
 DE Alpha-substituted short peptide.
 KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
 KW improved bioavailability.
 OS Synthetic.

RESULT 2
 AAR33008 ID AAR33008 standard; peptide: 5 AA.
 AC AAR33008;
 XX DT 25-MAR-2003 (revised)
 DT 02-APR-1993 (first entry)
 DE Alpha-substituted short peptide.
 KW CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia;
 KW improved bioavailability.
 OS Synthetic.
 XX FT Key Modified-site Location/Qualifiers
 FT FT Modified-site 2 /note= "alpha-Me-Phe"
 FT FT Modified-site 5 /note= "alpha-Me-Phe"

GenCore version 5.1.6
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OM protein - protein search, using SW model
Run on: October 26, 2005, 08:25:34 ; Search time 169 Seconds
15.150 Million cell updates/sec

Title:

Perfect score: 22

Sequence: 1 FXGLM 5

Scoring-table: BLOSUM62X Gapext: 0.5

Minimum_DB_seq_length: 0

Maximum_DB_seq_length: 11

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3223

Post-processing: Minimum Match 0% Listing first 150 summaries

Database: UniProt 03;*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------|--------------------------------|
| 1 | 22 | 100.0 | 10 | 1 TKNL_SCYCA | P08608 scyliorhinus |
| 2 | 22 | 100.0 | 10 | 1 TKNB_CHICK | P19851 gallus gallus |
| 3 | 22 | 100.0 | 10 | 1 TKNB_ONCMI | P28500 oncorynchus |
| 4 | 22 | 100.0 | 10 | 1 TKNB_RANCA | P22689 rana catesbeiana |
| 5 | 22 | 100.0 | 10 | 1 TKNB_RANRI | P23135 rana ridibunda |
| 6 | 22 | 100.0 | 10 | 1 TKNC_RANCA | P22690 rana catesbeiana |
| 7 | 22 | 100.0 | 10 | 1 TKNK_PIG | P07934 sus scrofa |
| 8 | 22 | 100.0 | 10 | 1 TKNK_RANRI | P67935 rana ridibunda |
| 9 | 22 | 100.0 | 10 | 1 TKN_PHYBI | P08610 phyllomedusa |
| 10 | 22 | 100.0 | 10 | 1 TKS1_AEDAE | P42634 aedes aegypti |
| 11 | 22 | 100.0 | 10 | 1 TKS2_AEDAE | P42635 aedes aegypti |
| 12 | 22 | 100.0 | 11 | 1 TKN1_PSEGU | P42986 pseudophryne |
| 13 | 22 | 100.0 | 11 | 1 TKN1_UPERIN | P08206 uperoleia rufa |
| 14 | 22 | 100.0 | 11 | 1 TKN1_UPERU | P08612 uperoleia rufa |
| 15 | 22 | 100.0 | 11 | 1 TKN2_PSEGU | P42987 pseudophryne |
| 16 | 22 | 100.0 | 11 | 1 TKN2_UPERU | P08616 uperoleia rufa |
| 17 | 22 | 100.0 | 11 | 1 TKN3_PSEGU | P42988 pseudophryne |
| 18 | 22 | 100.0 | 11 | 1 TKN4_PSEGU | P42989 pseudophryne |
| 19 | 22 | 100.0 | 11 | 1 TKN5_PSEGU | P42990 pseudophryne |
| 20 | 22 | 100.0 | 11 | 1 TKN6_CAVPO | P67932 cavia porcellus |
| 21 | 22 | 100.0 | 11 | 1 TKN6_CHICK | P19850 gallus gallus |
| 22 | 22 | 100.0 | 11 | 1 TKN6_GADMO | P28498 gadus morhua |
| 23 | 22 | 100.0 | 11 | 1 TKN6_HORSE | P67933 equus caballus |
| 24 | 22 | 100.0 | 11 | 1 TKN6_ONCMI | P28499 oncorynchus |
| 25 | 22 | 100.0 | 11 | 1 TKN6_RANCA | P22688 rana catesbeiana |
| 26 | 22 | 100.0 | 11 | 1 TKN6_RANRI | P22687 rana ridibunda |
| 27 | 22 | 100.0 | 11 | 1 TKN6_SCYCA | P41333 scyliorhinus |
| 28 | 22 | 100.0 | 11 | 1 TKN_ELECMO | P22933 eleotris cirrhosa |
| 29 | 22 | 100.0 | 11 | 1 TKN_ELEMO | P62934 eleotris moorii |
| 30 | 22 | 100.0 | 11 | 1 TKN_PHYFU | P08615 physalaemus |
| 31 | 22 | 100.0 | 11 | 2 Q9WAR8 | Q9WAR8 aedes aegypti |
| 32 | 17 | 77.3 | 10 | 2 Q61L97 | 061l97 nelisera gmeloides |
| 33 | 16 | 72.7 | 10 | 2 Q35013 | 035013 meloidogyne |
| 34 | 16 | 72.7 | 10 | 2 Q76ML8 | 076ml8 eurypharynx |
| 35 | 16 | 72.7 | 10 | 2 Q7M278 | 07m278 tritium tupeirae |
| 36 | 15 | 68.2 | 9 | 1 TRP4_LEUMA | P81736 leucophaea |
| 37 | 15 | 68.2 | 9 | 2 Q7M313 | 07m313 penaeus vannamei |
| 38 | 15 | 68.2 | 10 | 1 TRP6_LEUMA | P81738 leucophaea |
| 39 | 15 | 68.2 | 10 | 1 TRP7_LEUMA | P81739 leucophaea |
| 40 | 15 | 68.2 | 10 | 1 TRP8_LEUMA | P81740 leucophaea |
| 41 | 15 | 68.2 | 10 | 1 TRP9_LEUMA | P81741 leucophaea |
| 42 | 15 | 68.2 | 11 | 2 Q9E446 | 09r446 neisseria gonorrhoeae |
| 43 | 14 | 63.6 | 9 | 1 TKC1_CALVO | P41517 calliphora vicina |
| 44 | 14 | 63.6 | 9 | 1 TKU1_LOCHI | P16223 locusta migratoria |
| 45 | 14 | 63.6 | 9 | 2 Q85599 | 085599 moloney muridum |
| 46 | 14 | 63.6 | 10 | 1 TKU2_LOCHI | P16224 locusta migratoria |
| 47 | 14 | 63.6 | 10 | 1 TKU3_LOCHI | P30249 locusta migratoria |
| 48 | 14 | 63.6 | 10 | 1 TKU4_LOCHI | P26816 macrobrachium europaeum |
| 49 | 14 | 63.6 | 10 | 1 TRP5_LEUMA | P81737 leucophaea |
| 50 | 14 | 63.6 | 11 | 1 TKC2_CALVO | P41518 calliphora vicina |
| 51 | 13 | 59.1 | 5 | 1 TPIS_CANPES | P54714 canis familiaris |
| 52 | 13 | 59.1 | 7 | 1 PPH2_LYCES | P83379 lycopterus |
| 53 | 13 | 59.1 | 8 | 1 CCKN_DASVIT | P68125 dasypurus villosus |
| 54 | 13 | 59.1 | 8 | 1 CCKN_MAKEU | P84121 sporopteron |
| 55 | 13 | 59.1 | 8 | 1 TXVI_PHONII | P7m3p1 phoneutria brasiliensis |
| 56 | 13 | 59.1 | 8 | 2 Q9AVF3 | 09avf3 varanus kei |
| 57 | 13 | 59.1 | 8 | 2 P09258 | 09258 synecococcus |
| 58 | 13 | 59.1 | 9 | 1 CAER_PHYSA | 0712c4 physilomedusa |
| 59 | 13 | 59.1 | 9 | 1 FIBB_PAPRA | P84119 carcinus major |
| 60 | 13 | 59.1 | 9 | 1 FIBB_THEGE | P19342 theropithecus |
| 61 | 13 | 59.1 | 9 | 1 CCAP_TENNO | P84120 tenebrio molitor |
| 62 | 13 | 59.1 | 9 | 1 RE42_LITRU | P19345 erythrocebus patas |
| 63 | 13 | 59.1 | 9 | 1 SAMP_MUSICA | P7m3n6 gryllus bimaculatus |
| 64 | 13 | 59.1 | 9 | 1 Q7M3N6 | 07m3n6 gryllus bimaculatus |
| 65 | 13 | 59.1 | 9 | 1 FIBB_MACPEU | P19344 papio anubis |
| 66 | 13 | 59.1 | 9 | 1 FIBB_PAPPIN | P19343 papiro hamadryas |
| 67 | 13 | 59.1 | 9 | 1 RE42_LITRU | P19342 theropithecus |
| 68 | 13 | 59.1 | 9 | 1 Q7M3N6 | P82075 tenebrio molitor |
| 69 | 13 | 59.1 | 9 | 1 Q7M3N6 | P19345 macaca fasciata |
| 70 | 13 | 59.1 | 9 | 2 Q8MUN1 | P19344 papio anubis |
| 71 | 13 | 59.1 | 9 | 2 Q8MUN2 | P19343 papiro hamadryas |
| 72 | 13 | 59.1 | 9 | 2 Q8MUN3 | P19342 theropithecus |
| 73 | 13 | 59.1 | 9 | 2 Q8MUN4 | P19345 erythrocebus patas |
| 74 | 13 | 59.1 | 9 | 2 Q8MUN5 | P19346 gryllus bimaculatus |
| 75 | 13 | 59.1 | 9 | 2 Q8MUN6 | 07m3n6 actius azarae |
| 76 | 13 | 59.1 | 9 | 2 Q8MUN7 | 08mjn7 saimiri sciureus |
| 77 | 13 | 59.1 | 9 | 2 Q8MUN8 | 08mjn8 cebus apella |
| 78 | 13 | 59.1 | 9 | 2 Q8MUN9 | 08mjn9 atelopus fuscus |
| 79 | 13 | 59.1 | 9 | 2 Q7M2M7 | 07m2m7 bos taurus |
| 80 | 13 | 59.1 | 9 | 2 Q67AR4 | 067ar4 homo sapiens |
| 81 | 13 | 59.1 | 9 | 2 Q67AR6 | 067ar6 homo sapiens |
| 82 | 13 | 59.1 | 9 | 2 Q67AR7 | 067ar7 homo sapiens |
| 83 | 13 | 59.1 | 9 | 2 Q67AT1 | 067at1 homo sapiens |
| 84 | 13 | 59.1 | 9 | 2 Q67AT2 | 067at2 homo sapiens |
| 85 | 13 | 59.1 | 9 | 2 Q30790 | 030790 erwinia amylovora |
| 86 | 13 | 59.1 | 10 | 1 CAER_LITRA | P56264 litoria xanthochroa |
| 87 | 13 | 59.1 | 10 | 1 DY56_LIMSA | P82084 limnodynastes |
| 88 | 13 | 59.1 | 10 | 1 PPCK_FASIE | P80525 fasciolaria hebraica |
| 89 | 13 | 59.1 | 10 | 1 TKU1_UREIN | P40751 urechis unicinctus |
| 90 | 13 | 59.1 | 10 | 1 TKU2_UREIN | P40752 urechis unicinctus |
| 91 | 13 | 59.1 | 10 | 1 TP3_NICEL | P19118 nicotiana tabacum |
| 92 | 13 | 59.1 | 10 | 2 Q7M4X1 | 07m4x1 basidiobolus |
| 93 | 13 | 59.1 | 10 | 2 Q7M4X7 | 07m4x7 fusarium sp. |
| 94 | 13 | 59.1 | 10 | 2 Q725A2 | 0725a2 fasciolaria hebraica |
| 95 | 13 | 59.1 | 10 | 2 Q25355 | P25355 locusta migratoria |
| 96 | 13 | 59.1 | 10 | 2 Q23356 | 023356 locusta migratoria |
| 97 | 13 | 59.1 | 10 | 2 Q9BNBL | 095nbl euleptilis fuliginea |
| 98 | 13 | 59.1 | 10 | 2 Q6PD24 | 06pd24 bos taurus |
| 99 | 13 | 59.1 | 10 | 2 Q67014 | 06q11 bovus taurus |
| 100 | 13 | 59.1 | 10 | 2 Q6Q115 | 06q15 bos taurus |
| 101 | 13 | 59.1 | 10 | 2 Q64ET6 | 064et6 bos taurus |
| 102 | 13 | 59.1 | 10 | 2 Q62X62 | 06ex62 hypris slavicus |
| 103 | 13 | 59.1 | 10 | 2 Q71VN2 | 071vn2 mus musculus |
| 104 | 13 | 59.1 | 10 | 2 Q7LZC5 | 071zc5 kassina maculata |

OM protein - protein search, using SW model

Run on: October 26, 2005, 08:26:18 ; Search time 37 Seconds
 (without alignments)
 13.002 Million cell updates/sec

| | | | | |
|------------------|---|--------------------|-------|-------------|
| Title: | US-10-053-669-4 | | | |
| Scoring table: | PROSNC2DX | | | |
| Sequence: | 1 FXGLM 5 | | | |
| Post-processing: | Minimum DB-seq-length: 0 Maximum DB-seq length: 11 | | | |
| Database : | pir1;pir2;pir3;pir4; | | | |
| Result No. | Score | Query Match Length | DB ID | Description |
| 1 | 22 | 100.0 | 10 | SPPGNK |
| 2 | 22 | 100.0 | 10 | JN0024 |
| 3 | 22 | 100.0 | 10 | B49881 |
| 4 | 22 | 100.0 | 10 | A49881 |
| 5 | 22 | 100.0 | 10 | A24867 |
| 6 | 22 | 100.0 | 10 | S23187 |
| 7 | 22 | 100.0 | 10 | S23186 |
| 8 | 22 | 100.0 | 10 | S07202 |
| 9 | 22 | 100.0 | 10 | C61033 |
| 10 | 22 | 100.0 | 10 | B61033 |
| 11 | 22 | 100.0 | 10 | S27178 |
| 12 | 22 | 100.0 | 11 | A60154 |
| 13 | 22 | 100.0 | 11 | E00C |
| 14 | 22 | 100.0 | 11 | E00CC |
| 15 | 22 | 100.0 | 11 | SPHO |
| 16 | 22 | 100.0 | 11 | JN0023 |
| 17 | 22 | 100.0 | 11 | S33100 |
| 18 | 22 | 100.0 | 11 | S07203 |
| 19 | 22 | 100.0 | 11 | C60409 |
| 20 | 22 | 100.0 | 11 | E60409 |
| 21 | 22 | 100.0 | 11 | B60409 |
| 22 | 22 | 100.0 | 11 | F60409 |
| 23 | 22 | 100.0 | 11 | D60409 |
| 24 | 22 | 100.0 | 11 | S23108 |
| 25 | 22 | 100.0 | 11 | S23106 |
| 26 | 22 | 100.0 | 11 | S07201 |
| 27 | 22 | 100.0 | 11 | A61033 |
| 28 | 17 | 77.3 | 11 | PT049 |
| 29 | 16 | 72.7 | 10 | S19396 |

Total number of hits satisfying chosen parameters: 1328

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | |
|----------------------|----------------------|
| Met-enkephalin - b | Ig heavy chain-Arg |
| Ig heavy chain CDR | pev-tachykinin - p |
| Ig heavy chain CRD | tachykinin I - mig |
| tachykinin III - m | tachykinin IV - mi |
| cytocrom P450 A | tachykinin II - mi |
| tachykinin II - mi | IG heavy chain CRD |
| IG heavy chain CRD | halo-toxin - Pseud |
| halo-toxin - Pseud | 180K exoantigen - |
| 180K exoantigen - | IG mu chain D regi |
| IG mu chain D regi | cholecytokerinin - |
| cholecytokerinin - | cholecytokerinin - |
| cholecytokerinin - | polygalacturonase |
| Polygalacturonase | fibroblast growth |
| fibroblast growth | telomeric and tetr |
| telomeric and tetr | spasmogenic toxin |
| spasmogenic toxin | phyloacarulein - |
| phyloacarulein - | fibrinogen beta ch |
| fibrinogen beta ch | cardioactive pepti |
| cardioactive pepti | neuropeptide Gb3A |
| neuropeptide Gb3A | fibrinopeptide B - |
| fibrinopeptide B - | cardioactive pepti |
| cardioactive pepti | serum amyloid P-co |
| serum amyloid P-co | enamelin i - bovin |
| enamelin i - bovin | caerulein - frog (|
| caerulein - frog (| caerulein-like pep |
| caerulein-like pep | protein PII - curi |
| protein PII - curi | matrix metallopro |
| matrix metallopro | FC mu (IgM) recept |
| FC mu (IgM) recept | T-cell receptor al |
| T-cell receptor al | triose-phosphate i |
| triose-phosphate i | nuclease BNI (EC 3 |
| nuclease BNI (EC 3 | dihydroorotate (EC |
| dihydroorotate (EC | buccalin - Califor |
| buccalin - Califor | ieu-enkephalin - b |
| ieu-enkephalin - b | calliforamide 13 |
| calliforamide 13 | beta-neoendorphin |
| beta-neoendorphin | IG heavy chain CRD |
| IG heavy chain CRD | 19 heavy chain CRD |
| 19 heavy chain CRD | 27.5 structural p |
| 27.5 structural p | 27.5K structural p |
| 27.5K structural p | 28.5K structural p |
| 28.5K structural p | 28K structural pro |
| 28K structural pro | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | IG heavy chain CRD |
| IG heavy chain CRD | asparagine transami |
| asparagine transami | T-cell receptor be |
| T-cell receptor be | NADH 2 dehydrogenase |
| NADH 2 dehydrogenase | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | trichodecenin I - |
| trichodecenin I - | trichodecenin II - |
| trichodecenin II - | IG gamma chain C r |
| IG gamma chain C r | IG H chain V-D-J r |
| IG H chain V-D-J r | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |
| T-cell receptor be | T-cell receptor be |

Query Match 100 %; Score 22; DB 1; length 10;
 Best Local Similarity 80.0%; Pred. No. 21;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGLM 5
 Db 6 FVGLM 10

RESULT 2

JN0024 neurokinin A - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: JN0024
 R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
 Regul. Pept. 20, 171-180, 1988
 A;Title: [Arg]substance P and neurokinin A from chicken small intestine.
 A;Reference number: JN0023; MUID:88204263; PMID:2452461
 A;Accession: JN0024
 A;Molecule type: protein
 A;Residues: 1-10 <CON>
 A;Cross-references: UNIPROT:PI9851
 C;Superfamily: substance P precursor
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F;10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 100.0%; Score 22; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 21;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGLM 5
 Db 6 FVGLM 10

RESULT 3

B49581 sialokinin II - Yellow fever mosquito
 C;Species: Aedes aegypti (Yellow fever mosquito)
 C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
 C;Accession: B49581
 R;Champagne, D.B.; Ribeiro, J.M. Acad. Sci. U.S.A. 91, 138-142, 1994
 Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
 A;Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Acc
 A;Reference number: A49581; MUID:94105119; PMID:8278354
 A;Accession: A49581
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <CHA>
 A;Cross-references: UNIPROT:P42635
 A;Experimental source: Rockefeller, salivary gland
 A;Note: Sequence extracted from NCBI backbone (NCBIP:141842)

Query Match 100.0%; Score 22; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 21;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXGLM 5
 Db 6 FVGLM 10

RESULT 4

A49581 sialokinin I - yellow fever mosquito
 C;Species: Aedes aegypti (Yellow fever mosquito)
 C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49581
 R;Champagne, D.B.; Ribeiro, J.M. Acad. Sci. U.S.A. 91, 138-142, 1994
 Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994
 A;Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Acc
 A;Reference number: A49581; MUID:94105119; PMID:8278354

RESULT 1

SPPGNK
 neurokinin K - Pig
 C;Species: Sus scrofa domesticus (domestic Pig)
 C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
 C;Accession: A01560
 R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 114, 533-540, 1983
 A;Title: Neurokinin K, a novel mammalian tachykinin identified in porcine spinal cord.
 A;Reference number: A01560; MUID:83282812; PMID:6576785
 A;Accession: A01560
 A;Molecule type: protein
 A;Residues: 1-10 <KAN>
 A;Cross-references: UNIPROT:P01292
 A;Note: the structure of the peptide was confirmed by synthesis
 C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth muscle contraction.
 C;Superfamily: neurokinin B precursor
 C;Keywords: amidated carboxyl end; hormone; spinal cord
 F;10/Modified site: amidated carboxyl end (Met) #status experimental

GenCore version 5.1.6
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OM protein - protein search, using SW model
Run on: October 26, 2005, 08:31:09 ; Search time 162 Seconds
12.886 Million cell updates/sec

Title: US-10-053-669-4
Perfect score: 22
Sequence: 1 FXGLM 5

Scoring table: BLOSUM62DX Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 250346
Minimum DB seq length: 0

Maximum DB seq length: 11
Post-processing: Maximum-Match 0%
Listing first 150 summaries

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4. /cgn2_6/ptodata/1/pubpaas/US06_PUBCOMB.pep:
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7. /cgn2_6/ptodata/1/pubpaas/US07_NEW_PUB.pep:
8. /cgn2_6/ptodata/1/pubpaas/US08_PUBCOMB.pep:
9. /cgn2_6/ptodata/1/pubpaas/US09A_PUBCOMB.pep:
10. /cgn2_6/ptodata/1/pubpaas/US09B_PUBCOMB.pep:
11. /cgn2_6/ptodata/1/pubpaas/US09C_PUBCOMB.pep:
12. /cgn2_6/ptodata/1/pubpaas/US09_NEW_PUB.pep:
13. /cgn2_6/ptodata/1/pubpaas/US10A_PUBCOMB.pep:
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19. /cgn2_6/ptodata/1/pubpaas/US11B_PUBCOMB.pep:
20. /cgn2_6/ptodata/1/pubpaas/US11C_PUBCOMB.pep:
21. /cgn2_6/ptodata/1/pubpaas/US60_NEW_PUB.pep:
22. /cgn2_6/ptodata/1/pubpaas/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
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| 1 | 22 | 100.0 | 5 9 US-09-265-690C-1 | Sequence 1, Appli |
| 2 | 22 | 100.0 | 5 9 US-09-265-690C-4 | Sequence 4, Appli |
| 3 | 22 | 100.0 | 5 14 US-10-230-139-4 | Sequence 4, Appli |
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| 19 | 22 | 100.0 | 6 20 US-11-066-697-595 | Sequence 595, Appli |
| 20 | 22 | 100.0 | 6 20 US-11-066-697-597 | Sequence 597, Appli |
| 21 | 22 | 100.0 | 6 20 US-11-066-637-601 | Sequence 601, Appli |
| 22 | 22 | 100.0 | 7 14 US-10-036-542-110 | Sequence 110, Appli |
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Publication No. US20010051345A1
 FILE REFERENCE: 1427001
 CURRENT APPLICATION NUMBER: US/09/265,690C
 CURRENT FILING DATE: 1999-03-10
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 1
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (15)..(15)
 OTHER INFORMATION: AMIDATION
 ; US-09-265,690C-1
 Query Match Local Similarity Score 22; DB 9; Length 5;
 Best Local Simililarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXGLM 5
 Db 1 FXGLM 5

RESULT 2
 US-09-265-690C-4
 Sequence 4, Application US/09265690C
 Publication No. US20010051345A1
 ; GENERAL INFORMATION:
 APPLICANT: Wells, Ibert
 TITLE OF INVENTION: Method for Detecting Deficient Cellular Membrane Tightly Bound Ma
 FILE REFERENCE: 1427001
 CURRENT APPLICATION NUMBER: US/09/265,690C
 CURRENT FILING DATE: 1999-03-10
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 4
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
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 LOCATION: (5)..(5)
 OTHER INFORMATION: AMIDATION
 NAME/KEY: VARIANT
 LOCATION: (2)..(2)
 OTHER INFORMATION: "X" may be either Phe or Val.
 US-09-265-690C-4

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 Best Local Simililarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FXGLM 5
 Db 1 FXGLM 5

RESULT 3
 US-09-265-690C-4

ALIGNMENTS

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Gencore version 5.1.6

Run on: October 26, 2005, 08:30:04 ; Search time 21 Seconds
 (without alignments)
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Title: Perfect score: US-10-053-669-4

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries

Database : Issued Patents AA:*

Minimum DB seq length: 0 Maximum DB seq length: 11

Total number of hits satisfying chosen parameters: 125705

Score: 513545 seqs, 7465964 residues

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| 54 | 22 | 100.0 | 10 | 1 | US-08-39B-91B-4 | Sequence 12, Appli |
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101 22 100.0 11 1 US-08-428-498-17 Sequence 17, Appl
 102 22 100.0 11 1 US-03-255-272-6 Sequence 6, Appl
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 106 22 100.0 11 1 US-03-122-659A-1 Sequence 2, Appl
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 131 22 100.0 11 2 US-08-848-766A-1 Sequence 1, Appl
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 135 22 100.0 11 3 US-09-214-614-1 Sequence 7, Appl
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 137 22 100.0 11 4 US-08-153-847-2 Sequence 9, Appl
 138 22 100.0 11 4 US-09-635-266-1 Sequence 10, Appl
 139 22 100.0 11 4 US-03-570-022-4 Sequence 5, Appl
 140 22 100.0 11 4 US-03-570-022-5 Sequence 6, Appl
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 146 22 100.0 11 4 US-10-003-593-4 Sequence 1, Appl
 147 22 100.0 11 4 US-10-629-642A-1 Sequence 21, Appl
 148 22 100.0 11 4 US-10-230-133-1 Sequence 1, Appl
 149 22 100.0 11 4 US-09-428-692-21 Sequence 1, Appl
 150 22 100.0 11 4 US-09-285-377A-1

ALIGNMENTS

RESULT 1
 US-07-753-909B-3 Application US/07753909B
 ; Sequence 3, Application US/07753909B
 ; Patent No. 5314632
 ; GENERAL INFORMATION:
 ; APPLICANT: Conlon, Michael J.
 ; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Zarley, McKee, Voorhees, and Sease
 ; STREET: 801 Grand, Suite 3200
 ; CITY: Des Moines
 ; STATE: Iowa
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/934,553
 ; FILING DATE: 19920821
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/705,071
 ; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FENTRESS, SUSAN B
 ; REGISTRATION NUMBER: 31,327
 ; REFERENCE/DOCKET NUMBER: NU-9033CIP
 ; TELECOMMUNICATION INFORMATION:

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: FR 9106759
 FILING DATE: 04-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Sease, Edmund J.
 REGISTRATION NUMBER: 24,741
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (515)-288-1338
 TELEFAX: (515)-288-3667
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: C-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rana ridibunda
 DEVELOPMENTAL STAGE: adult
 TISSUE TYPE: brain
 US-07-753-909B-3
 Query Match Similarity Score 22; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 FXGLM 5
 DB 1 FXGLM 5
 ; Sequence 2, Application US/07934553
 ; Patent No. 5314690
 ; GENERAL INFORMATION:
 ; APPLICANT: PATTERSON, ROY
 ; APPLICANT: HARRIS, KATHLEEN E
 ; TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGB
 ; TITLE OF INVENTION: ANTI-BODIES TO SPECIFIC ALLERGENS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: TILTON, FALLON, LUNGMIUS & CHESTNUT
 ; STREET: 100 SOUTH WACKER DRIVE
 ; CITY: CHICAGO
 ; STATE: ILLINOIS
 ; COUNTRY: USA
 ; ZIP: 60606-4002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/934,553
 ; FILING DATE: 19920821
 ; CLASSIFICATION: 424
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/705,071
 ; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FENTRESS, SUSAN B
 ; REGISTRATION NUMBER: 31,327
 ; REFERENCE/DOCKET NUMBER: NU-9033CIP
 ; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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OM protein - protein search, using SW model
Run on: October 26, 2005, 08:21:45 ; Search time 162 Seconds
11.937 Million cell updates/sec

Title:

Perfect score: US2005053-669-4

Sequence:
1 PXGLM 5Scoring table:
BioSpherixDBX

Gapop 10.0 , Gapext 0.5

Searched:

2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 494136

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database: ~~bioSpherixDBX~~ AugeneBGP_J6dec04: *Database: ~~bioSpherixDBX~~ GenesedB1990g: *Database: ~~bioSpherixDBX~~ GenesedB1990b: *Database: ~~bioSpherixDBX~~ GenesedB2008b: *Database: ~~bioSpherixDBX~~ GenesedB2013b: *Database: ~~bioSpherixDBX~~ GenesedB2008a: *Database: ~~bioSpherixDBX~~ GenesedB2003b: *Database: ~~bioSpherixDBX~~ GenesedB2004b: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 19 | 22 | 100.0 | 5 4 | Aab82431 Fluorinat |
| 20 | 22 | 100.0 | 5 4 | Aab91428 Tachykini |
| 21 | 22 | 100.0 | 5 4 | Aab70556 Octopus t |
| 22 | 22 | 100.0 | 5 5 | Aau10800 Human bet |
| 23 | 22 | 100.0 | 5 5 | ABP10088 Substance |
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| 27 | 22 | 100.0 | 5 7 | ADB94203 High acti |
| 28 | 22 | 100.0 | 5 7 | ADB92530 Substance |
| 29 | 22 | 100.0 | 5 8 | ADM12180 Tachykini |
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| 38 | 22 | 100.0 | 6 2 | Aar07897 Cyclicopept |
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| 45 | 22 | 100.0 | 6 2 | Aaw92706 Human tac |
| 46 | 22 | 100.0 | 6 2 | Aaw92659 Human tac |
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| 48 | 22 | 100.0 | 6 3 | Aav67575 P artagon |
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| 53 | 22 | 100.0 | 6 4 | Aab91421 Tachykini |
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| 57 | 22 | 100.0 | 6 4 | Aab74306 Peptidic a |
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| 72 | 22 | 100.0 | 7 4 | Aab80324 Human pro |
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| 103 | 22 | 9 | AAB9146 |
| 104 | 22 | 9 | AAB91369 |
| 105 | 22 | 9 | AAG9348 |
| 106 | 22 | 9 | ADP92528 |
| 107 | 22 | 9 | ADN5076 |
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| 130 | 22 | 10 | AAB91398 |
| 131 | 22 | 10 | AAB91355 |
| 132 | 22 | 10 | AAB91397 |
| 133 | 22 | 10 | AAB91370 |
| 134 | 22 | 10 | AAB91368 |
| 135 | 22 | 10 | AAB91445 |
| 136 | 22 | 10 | AAB91356 |
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| 140 | 22 | 10 | AAG64746 |
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| 144 | 22 | 10 | ABB99004 |
| 145 | 22 | 10 | ABB99003 |
| 146 | 22 | 10 | ABG76704 |
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| 148 | 22 | 10 | ADC63998 |
| 149 | 22 | 10 | ADC63999 |
| 150 | 22 | 10 | ADG89837 |
| | SQ | Sequence 5 AA; | |
| | Query Match | 100.0% | Score 22; DB 2; Length 5; |
| | Best Local Similarity | 80.0% | Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0; |
| | Matches | 4 | Conservative; 1; Mismatches 0; Indels 0; Gaps 0; |
| | Qy | 1 | FXGLM 5 |
| | D _b | 1 | FFGLM 5 |
| | RESULT 2 | | |
| ID | AAR33008 | | |
| ID | AAR33008 standard; peptide; 5 AA. | | |
| XX | | | |
| AC | AAR33008; | | |
| XX | | | |
| AC | AAR33008; | | |
| XX | | | |
| DT | 25-MAR-2003 (revised) | | |
| DT | 02-APR-1993 (first entry) | | |
| DE | Alpha -substituted short peptide. | | |
| XX | | | |
| DE | Alpha -substituted short peptide. | | |
| XX | | | |
| KW | CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia; improved bioavailability. | | |
| XX | | | |
| OS | Synthetic. | | |
| | RESULT 1 | | |
| ID | AAR33009 | | |
| ID | AAR33009 standard; peptide; 5 AA. | | |
| XX | | | |
| AC | AAR33009; | | |
| XX | | | |
| DT | 25-MAR-2003 (revised) | | |
| DT | 02-APR-1993 (first entry) | | |
| DE | Alpha -substituted short peptide. | | |
| XX | | | |
| KW | CCK; neuropeptide; endorphin; hormone; LHRH; contraception; analgesia; improved bioavailability. | | |
| XX | | | |
| OS | Synthetic. | | |